

## SEQUENCE LISTING

<110> Dana-Farber Cancer Institute, Inc.  
 <120> REGULATION OF IMMUNE RESPONSES BY ATTRACTIN  
 <130> 00530/089W01  
 <150> US 60/100,137  
 <151> 1998-09-14  
 <160> 25  
 <170> FastSEQ for Windows Version 3.0  
 <210> 1  
 <211> 3597  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> CDS  
 <222> (1)...(3594)

<400> 1  
 atg gtg gcc gca gcg gcg gca act gag gca agg ctg agg agg agg acg 48  
 Met Val Ala Ala Ala Ala Ala Thr Glu Ala Arg Leu Arg Arg Arg Thr  
 1 5 10 15  
 gcg gcg acg gca gcg ctc gcg ggc agg agc ggc ggc ccg cac tgt gtc 96  
 Ala Ala Thr Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Cys Val  
 20 25 30  
 aac ggc ggt cgc tgc aac cct ggc acc ggc cag tgc gtc tgc ccc gcc 144  
 Asn Gly Gly Arg Cys Asn Pro Gly Thr Gly Gln Cys Val Cys Pro Ala  
 35 40 45  
 ggc tgg gtg ggc gag caa tgc cag cac tgc ggc ggc cgc ttc aga cta 192  
 Gly Trp Val Gly Glu Gln Cys Gln His Cys Gly Gly Arg Phe Arg Leu  
 50 55 60  
 act gga tct tct ggc ttt gtg aca gat gga cct gga aat tat aaa tac 240  
 Thr Gly Ser Ser Gly Phe Val Thr Asp Gly Pro Gly Asn Tyr Lys Tyr  
 65 70 75 80  
 aaa acg aag tgc acg tgg ctc att gaa gga cag cca aat aga ata atg 288  
 Lys Thr Lys Cys Thr Trp Leu Ile Glu Gly Gln Pro Asn Arg Ile Met  
 85 90 95  
 aga ctt cgt ttc aat cat ttt gct aca gag tgt agt tgg gac cat tta 336  
 Arg Leu Arg Phe Asn His Phe Ala Thr Glu Cys Ser Trp Asp His Leu  
 100 105 110  
 tat gtt tat gat ggc gac tca att tat gca ccg cta gtt gct gca ttt 384  
 Tyr Val Tyr Asp Gly Asp Ser Ile Tyr Ala Pro Leu Val Ala Ala Phe  
 115 120 125  
 agt ggc ctc att gtt cct gag aga gat ggc aat gag act gtc cct gag 432  
 Ser Gly Leu Ile Val Pro Glu Arg Asp Gly Asn Glu Thr Val Pro Glu  
 130 135 140  
 gtt gtt gcc aca tca ggt tat gcc ttg ctg cat ttt ttt agt gat gct 480  
 Val Val Ala Thr Ser Gly Tyr Ala Leu Leu His Phe Phe Ser Asp Ala  
 145 150 155 160

gct tat aat ttg act gga ttt aat att act tac agt ttt gat atg tgt Ala Tyr Asn Leu Thr Gly Phe Asn Ile Thr Tyr Ser Phe Asp Met Cys 165 170 175	528
cca aat aac tgc tca ggc cga gga gag tgt aag atc agt aat agc agc Pro Asn Asn Cys Ser Gly Arg Gly Glu Cys Lys Ile Ser Asn Ser Ser 180 185 190	576
gat act gtt gaa tgt gaa tgt tct gaa aac tgg aaa ggt gaa gca tgt Asp Thr Val Glu Cys Glu Cys Ser Glu Asn Trp Lys Gly Glu Ala Cys 195 200 205	624
gac att cct cac tgt aca gac aac tgt ggt ttt cct cat cga ggc atc Asp Ile Pro His Cys Thr Asp Asn Cys Gly Phe Pro His Arg Gly Ile 210 215 220	672
tgc aat tca agt gat gtc aga gga tgc tcc tgc ttc tca gac tgg cag Cys Asn Ser Ser Asp Val Arg Gly Cys Ser Cys Phe Ser Asp Trp Gln 225 230 235 240	720
ggt cct gga tgt tca gtt cct gta cca gct aac cag tca ttt tgg act Gly Pro Gly Cys Ser Val Pro Val Pro Ala Asn Gln Ser Phe Trp Thr 245 250 255	768
cga gag gaa tat tct aac tta aag ctc ccc aga gca tct cat aaa gct Arg Glu Glu Tyr Ser Asn Leu Lys Leu Pro Arg Ala Ser His Lys Ala 260 265 270	816
gtg gtc aat gga aac att atg tgg gtt gtt gga gga tat atg ttc aac Val Val Asn Gly Asn Ile Met Trp Val Val Gly Gly Tyr Met Phe Asn 275 280 285	864
cac tca gat tat aac atg gtt cta gcg tat gac ctt gct tct agg gag His Ser Asp Tyr Asn Met Val Leu Ala Tyr Asp Leu Ala Ser Arg Glu 290 295 300	912
tgg ctt cca cta aac cgt tct gtg aac aat gtg gtt gtt aga tat ggt Trp Leu Pro Leu Asn Arg Ser Val Asn Asn Val Val Val Arg Tyr Gly 305 310 315 320	960
cat tct ttg gca tta tac aag gat aaa att tac atg tat gga gga aaa His Ser Leu Ala Leu Tyr Lys Asp Lys Ile Tyr Met Tyr Gly Gly Lys 325 330 335	1008
att gat tca act ggg aat gtg acc aat gag ttg aga gtt ttt cac att Ile Asp Ser Thr Gly Asn Val Thr Asn Glu Leu Arg Val Phe His Ile 340 345 350	1056
cat aat gag tca tgg gtg ttg ttg acc cct aag gca aag gag cag tat His Asn Glu Ser Trp Val Leu Leu Thr Pro Lys Ala Lys Glu Gln Tyr 355 360 365	1104
gca gtg gtt ggg cac tct gca cac att gtt aca ctg aag aat ggc cga Ala Val Val Gly His Ser Ala His Ile Val Thr Leu Lys Asn Gly Arg 370 375 380	1152
gtg gtc atg ctg gtc atc ttt ggt cac tgc cct ctc tat gga tat ata Val Val Met Leu Val Ile Phe Gly His Cys Pro Leu Tyr Gly Tyr Ile 385 390 395 400	1200
agc aat gtg cag gaa tat gat ttg gat aag aac aca tgg agt ata tta Ser Asn Val Gln Glu Tyr Asp Leu Asp Lys Asn Thr Trp Ser Ile Leu 405 410 415	1248
cac acc cag ggt gcc ctt gtg caa ggg ggt tac ggc cat agc agt gtt His Thr Gln Gly Ala Leu Val Gln Gly Gly Tyr Gly His Ser Ser Val 420 425 430	1296

tac gac cat agg acc agg gcc cta tac gtt cat ggt ggc tac aag gct Tyr Asp His Arg Thr Arg Ala Leu Tyr Val His Gly Gly Tyr Lys Ala 435 440 445	1344
ttc agt gcc aat aag tac cgg ctt gca gat gat ctc tac cga tat gat Phe Ser Ala Asn Lys Tyr Arg Leu Ala Asp Asp Leu Tyr Arg Tyr Asp 450 455 460	1392
gtg gat acc cag atg tgg acc att ctt aag gac agc cga ttt ttc cgt Val Asp Thr Gln Met Trp Thr Ile Leu Lys Asp Ser Arg Phe Phe Arg 465 470 475 480	1440
tac ttg cac aca gct gtg ata gtg agt gga acc atg ctg gtg ttt ggg Tyr Leu His Thr Ala Val Ile Val Ser Gly Thr Met Leu Val Phe Gly 485 490 495	1488
gga aac aca cac aat gac aca tct atg agc cat ggc gcc aaa tgc ttc Gly Asn Thr His Asn Asp Thr Ser Met Ser His Gly Ala Lys Cys Phe 500 505 510	1536
tct tca gat ttc atg gcc tat gac att gcc tgt gac cgc tgg tca gtg Ser Ser Asp Phe Met Ala Tyr Asp Ile Ala Cys Asp Arg Trp Ser Val 515 520 525	1584
ctt ccc aga cct gat tcc acc atg atg tca aca gat ttg gcc att cca Leu Pro Arg Pro Asp Ser Thr Met Met Ser Thr Asp Leu Ala Ile Pro 530 535 540	1632
gca gtc tta cac aac agc acc atg tat gtg ttc ggt ggt ttc aat agt Ala Val Leu His Asn Ser Thr Met Tyr Val Phe Gly Gly Phe Asn Ser 545 550 555 560	1680
ctc ctc ctc agc gac atc ctg gta ttc acc tcg gaa cag tgt gat gcg Leu Leu Leu Ser Asp Ile Leu Val Phe Thr Ser Glu Gln Cys Asp Ala 565 570 575	1728
cat cgg agt gaa gcc gct tgt tta gca gca gga cct ggt att cgg tgt His Arg Ser Glu Ala Ala Cys Leu Ala Ala Gly Pro Gly Ile Arg Cys 580 585 590	1776
gtg tgg aac aca ggg tcg tct cag tgt atc tcg tgg gcg ctg gca act Val Trp Asn Thr Gly Ser Ser Gln Cys Ile Ser Trp Ala Leu Ala Thr 595 600 605	1824
gat gaa caa gaa gaa aag tta aaa tca gaa tgt ttt tcc aaa aga act Asp Glu Gln Glu Glu Lys Leu Lys Ser Glu Cys Phe Ser Lys Arg Thr 610 615 620	1872
ctt gac cat gac aga tgt gac cag cac aca gat tgt tac agc tgc aca Leu Asp His Asp Arg Cys Asp Gln His Thr Asp Cys Tyr Ser Cys Thr 625 630 635 640	1920
gcc aac acc aat gac tgc cac tgg tgc aat gac cat tgt gtc ccc agg Ala Asn Thr Asn Asp Cys His Trp Cys Asn Asp His Cys Val Pro Arg 645 650 655	1968
aac cac agc tgc tca gaa ggc cag atc tcc att ttt agg tat gag aat Asn His Ser Cys Ser Glu Gly Gln Ile Ser Ile Phe Arg Tyr Glu Asn 660 665 670	2016
tgc ccc aag gat aac cct atg tac tac tgt aac aag aag acc agc tgc Cys Pro Lys Asp Asn Pro Met Tyr Tyr Cys Asn Lys Lys Thr Ser Cys 675 680 685	2064

agg agc tgt gcc ctg gac cag aac tgc cag tgg gag ccc cgg aat cag Arg Ser Cys Ala Leu Asp Gln Asn Cys Gln Trp Glu Pro Arg Asn Gln 690 695 700	2112
gag tgc att gcc ctg ccc gaa aat atc tgt ggc att ggc tgg cat ttg Glu Cys Ile Ala Leu Pro Glu Asn Ile Cys Gly Ile Gly Trp His Leu 705 710 715 720	2160
gtt gga aac tca tgt ttg aaa att act act gcc aag gag aat tat gac Val Gly Asn Ser Cys Leu Lys Ile Thr Thr Ala Lys Glu Asn Tyr Asp 725 730 735	2208
aat gct aaa ttg ttc tgt agg aac cac aat gcc ctt ttg gct tct ctt Asn Ala Lys Leu Phe Cys Arg Asn His Asn Ala Leu Leu Ala Ser Leu 740 745 750	2256
aca acc cag aag aag gta gaa ttt gtc ctt aag cag ctg cga ata atg Thr Thr Gln Lys Lys Val Glu Phe Val Leu Lys Gln Leu Arg Ile Met 755 760 765	2304
cag tca tct cag agc atg tcc aag ctc acc tta acc cca tgg gtc ggc Gln Ser Ser Gln Ser Met Ser Lys Leu Thr Leu Thr Pro Trp Val Gly 770 775 780	2352
ctt cgg aag atc aat gtg tcc tac tgg tgc tgg gaa gat atg tcc cca Leu Arg Lys Ile Asn Val Ser Tyr Trp Cys Trp Glu Asp Met Ser Pro 785 790 795 800	2400
ttt aca aat agt tta cta cag tgg atg ccg tct gag ccc agt gat gct Phe Thr Asn Ser Leu Leu Gln Trp Met Pro Ser Glu Pro Ser Asp Ala 805 810 815	2448
gga ttc tgt gga att tta tca gaa ccc agt act cgg gga ctg aag gct Gly Phe Cys Gly Ile Leu Ser Glu Pro Ser Thr Arg Gly Leu Lys Ala 820 825 830	2496
gca acc tgc atc aac cca ctc aat ggt agt gtc tgt gaa agg cct gca Ala Thr Cys Ile Asn Pro Leu Asn Gly Ser Val Cys Glu Arg Pro Ala 835 840 845	2544
aac cac agt gct aag cag tgc cgg aca cca tgt gcc ttg agg aca gca Asn His Ser Ala Lys Gln Cys Arg Thr Pro Cys Ala Leu Arg Thr Ala 850 855 860	2592
tgt gga gat tgc acc agc ggc agc tct gag tgc atg tgg tgc agc aac Cys Gly Asp Cys Thr Ser Gly Ser Ser Glu Cys Met Trp Cys Ser Asn 865 870 875 880	2640
atg aag cag tgt gtg gac tcc aat gcc tat gtg gcc tcc ttc cct ttt Met Lys Gln Cys Val Asp Ser Asn Ala Tyr Val Ala Ser Phe Pro Phe 885 890 895	2688
ggc cag tgt atg gaa tgg tat acg atg agc acc tgc ccc cct gaa aat Gly Gln Cys Met Glu Trp Tyr Thr Met Ser Thr Cys Pro Pro Glu Asn 900 905 910	2736
tgt tca ggc tac tgt acc tgt agt cat tgc ttg gag caa cca ggc tgt Cys Ser Gly Tyr Cys Thr Cys Ser His Cys Leu Glu Gln Pro Gly Cys 915 920 925	2784
ggc tgg tgt act gat ccc agc aat act ggc aaa ggg aaa tgc ata gag Gly Trp Cys Thr Asp Pro Ser Asn Thr Gly Lys Gly Lys Cys Ile Glu 930 935 940	2832
ggt tcc tat aaa gga cca gtg aag atg cct tgc caa gcc cct aca gga Gly Ser Tyr Lys Gly Pro Val Lys Met Pro Ser Gln Ala Pro Thr Gly 945 950 955 960	2880

aat ttc tat cca cag ccc ctg ctc aat tcc agc atg tgt cta gag gac 2928  
 Asn Phe Tyr Pro Gln Pro Leu Leu Asn Ser Ser Met Cys Leu Glu Asp  
 965 970 975

agc aga tac aac tgg tct ttc att cac tgt cca gct tgc caa tgc aac 2976  
 Ser Arg Tyr Asn Trp Ser Phe Ile His Cys Pro Ala Cys Gln Cys Asn  
 980 985 990

ggc cac agt aaa tgc atc aat cag agc atc tgt gag aag tgt gag aac 3024  
 Gly His Ser Lys Cys Ile Asn Gln Ser Ile Cys Glu Lys Cys Glu Asn  
 995 1000 1005

ctg acc aca ggc aag cac tgc gag acc tgc ata tct ggc ttc tac ggt 3072  
 Leu Thr Thr Gly Lys His Cys Glu Thr Cys Ile Ser Gly Phe Tyr Gly  
 1010 1015 1020

gat ccc acc aat gga ggg aaa tgt cag cca tgc aag tgc aat ggg cac 3120  
 Asp Pro Thr Asn Gly Gly Lys Cys Gln Pro Cys Lys Cys Asn Gly His  
 1025 1030 1035 1040

gcg tct ctg tgc aac acc aac acg ggc aag tgc ttc tgc acc acc aag 3168  
 Ala Ser Leu Cys Asn Thr Asn Thr Gly Lys Cys Phe Cys Thr Thr Lys  
 1045 1050 1055

ggc gtc aag ggg gac gag tgc cag cta tgt gag gta gaa aat cga tac 3216  
 Gly Val Lys Gly Asp Glu Cys Gln Leu Cys Glu Val Glu Asn Arg Tyr  
 1060 1065 1070

caa gga aac cct ctc aga gga aca tgt tat tat act ctt ctt att gac 3264  
 Gln Gly Asn Pro Leu Arg Gly Thr Cys Tyr Tyr Thr Leu Ile Asp  
 1075 1080 1085

tat cag ttc acc ttt agt cta tcc cag gaa gat gat cgc tat tac aca 3312  
 Tyr Gln Phe Thr Phe Ser Leu Ser Gln Glu Asp Asp Arg Tyr Tyr Thr  
 1090 1095 1100

gct atc aat ttt gtg gct act cct gac gaa caa aac agg gat ttg gac 3360  
 Ala Ile Asn Phe Val Ala Thr Pro Asp Glu Gln Asn Arg Asp Leu Asp  
 1105 1110 1115 1120

atg ttc atc aat gcc tcc aag aat ttc aac ctc aac atc acc tgg gct 3408  
 Met Phe Ile Asn Ala Ser Lys Asn Phe Asn Leu Asn Ile Thr Trp Ala  
 1125 1130 1135

gcc agt ttc tca gct gga acc cag gct gga gaa gag atg cct gtt gtt 3456  
 Ala Ser Phe Ser Ala Gly Thr Gln Ala Gly Glu Glu Met Pro Val Val  
 1140 1145 1150

tca aaa acc aac att aag gag tac aaa gat agt ttc tct aat gag aag 3504  
 Ser Lys Thr Asn Ile Lys Glu Tyr Lys Asp Ser Phe Ser Asn Glu Lys  
 1155 1160 1165

ttt gat ttt cgc aac cac cca aat atc act ttc ttt gtt tat gtc agt 3552  
 Phe Asp Phe Arg Asn His Pro Asn Ile Thr Phe Phe Val Tyr Val Ser  
 1170 1175 1180

aat ttc acc tgg ccc atc aaa att cag gtg caa act gaa caa 3594  
 Asn Phe Thr Trp Pro Ile Lys Ile Gln Val Gln Thr Glu Gln  
 1185 1190 1195

tga 3597

<210> 2  
 <211> 1198  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
Met Val Ala Ala Ala Ala Thr Glu Ala Arg Leu Arg Arg Arg Thr  
1 5 10 15  
Ala Ala Thr Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Cys Val  
20 25 30  
Asn Gly Gly Arg Cys Asn Pro Gly Thr Gly Gln Cys Val Cys Pro Ala  
35 40 45  
Gly Trp Val Gly Glu Gln Cys Gln His Cys Gly Gly Arg Phe Arg Leu  
50 55 60  
Thr Gly Ser Ser Gly Phe Val Thr Asp Gly Pro Gly Asn Tyr Lys Tyr  
65 70 75 80  
Lys Thr Lys Cys Thr Trp Leu Ile Glu Gly Gln Pro Asn Arg Ile Met  
85 90 95  
Arg Leu Arg Phe Asn His Phe Ala Thr Glu Cys Ser Trp Asp His Leu  
100 105 110  
Tyr Val Tyr Asp Gly Asp Ser Ile Tyr Ala Pro Leu Val Ala Ala Phe  
115 120 125  
Ser Gly Leu Ile Val Pro Glu Arg Asp Gly Asn Glu Thr Val Pro Glu  
130 135 140  
Val Val Ala Thr Ser Gly Tyr Ala Leu Leu His Phe Phe Ser Asp Ala  
145 150 155 160  
Ala Tyr Asn Leu Thr Gly Phe Asn Ile Thr Tyr Ser Phe Asp Met Cys  
165 170 175  
Pro Asn Asn Cys Ser Gly Arg Gly Glu Cys Lys Ile Ser Asn Ser Ser  
180 185 190  
Asp Thr Val Glu Cys Glu Cys Ser Glu Asn Trp Lys Gly Glu Ala Cys  
195 200 205  
Asp Ile Pro His Cys Thr Asp Asn Cys Gly Phe Pro His Arg Gly Ile  
210 215 220  
Cys Asn Ser Ser Asp Val Arg Gly Cys Ser Cys Phe Ser Asp Trp Gln  
225 230 235 240  
Gly Pro Gly Cys Ser Val Pro Val Pro Ala Asn Gln Ser Phe Trp Thr  
245 250 255  
Arg Glu Glu Tyr Ser Asn Leu Lys Leu Pro Arg Ala Ser His Lys Ala  
260 265 270  
Val Val Asn Gly Asn Ile Met Trp Val Val Gly Gly Tyr Met Phe Asn  
275 280 285  
His Ser Asp Tyr Asn Met Val Leu Ala Tyr Asp Leu Ala Ser Arg Glu  
290 295 300  
Trp Leu Pro Leu Asn Arg Ser Val Asn Asn Val Val Val Arg Tyr Gly  
305 310 315 320  
His Ser Leu Ala Leu Tyr Lys Asp Lys Ile Tyr Met Tyr Gly Gly Lys  
325 330 335  
Ile Asp Ser Thr Gly Asn Val Thr Asn Glu Leu Arg Val Phe His Ile  
340 345 350  
His Asn Glu Ser Trp Val Leu Leu Thr Pro Lys Ala Lys Glu Gln Tyr  
355 360 365  
Ala Val Val Gly His Ser Ala His Ile Val Thr Leu Lys Asn Gly Arg  
370 375 380  
Val Val Met Leu Val Ile Phe Gly His Cys Pro Leu Tyr Gly Tyr Ile  
385 390 395 400  
Ser Asn Val Gln Glu Tyr Asp Leu Asp Lys Asn Thr Trp Ser Ile Leu  
405 410 415  
His Thr Gln Gly Ala Leu Val Gln Gly Gly Tyr Gly His Ser Ser Val  
420 425 430  
Tyr Asp His Arg Thr Arg Ala Leu Tyr Val His Gly Gly Tyr Lys Ala  
435 440 445  
Phe Ser Ala Asn Lys Tyr Arg Leu Ala Asp Asp Leu Tyr Arg Tyr Asp  
450 455 460  
Val Asp Thr Gln Met Trp Thr Ile Leu Lys Asp Ser Arg Phe Phe Arg  
465 470 475 480  
Tyr Leu His Thr Ala Val Ile Val Ser Gly Thr Met Leu Val Phe Gly  
485 490 495  
Gly Asn Thr His Asn Asp Thr Ser Met Ser His Gly Ala Lys Cys Phe  
500 505 510  
Ser Ser Asp Phe Met Ala Tyr Asp Ile Ala Cys Asp Arg Trp Ser Val  
515 520 525

Leu Pro Arg Pro Asp Ser Thr Met Met Ser Thr Asp Leu Ala Ile Pro  
 530 535 540  
 Ala Val Leu His Asn Ser Thr Met Tyr Val Phe Gly Gly Phe Asn Ser  
 545 550 555 560  
 Leu Leu Leu Ser Asp Ile Leu Val Phe Thr Ser Glu Gln Cys Asp Ala  
 565 570 575  
 His Arg Ser Glu Ala Ala Cys Leu Ala Ala Gly Pro Gly Ile Arg Cys  
 580 585 590  
 Val Trp Asn Thr Gly Ser Ser Gln Cys Ile Ser Trp Ala Leu Ala Thr  
 595 600 605  
 Asp Glu Gln Glu Glu Lys Leu Lys Ser Glu Cys Phe Ser Lys Arg Thr  
 610 615 620  
 Leu Asp His Asp Arg Cys Asp Gln His Thr Asp Cys Tyr Ser Cys Thr  
 625 630 635 640  
 Ala Asn Thr Asn Asp Cys His Trp Cys Asn Asp His Cys Val Pro Arg  
 645 650 655  
 Asn His Ser Cys Ser Glu Gly Gln Ile Ser Ile Phe Arg Tyr Glu Asn  
 660 665 670  
 Cys Pro Lys Asp Asn Pro Met Tyr Tyr Cys Asn Lys Lys Thr Ser Cys  
 675 680 685  
 Arg Ser Cys Ala Leu Asp Gln Asn Cys Gln Trp Glu Pro Arg Asn Gln  
 690 695 700  
 Glu Cys Ile Ala Leu Pro Glu Asn Ile Cys Gly Ile Gly Trp His Leu  
 705 710 715 720  
 Val Gly Asn Ser Cys Leu Lys Ile Thr Thr Ala Lys Glu Asn Tyr Asp  
 725 730 735  
 Asn Ala Lys Leu Phe Cys Arg Asn His Asn Ala Leu Leu Ala Ser Leu  
 740 745 750  
 Thr Thr Gln Lys Lys Val Glu Phe Val Leu Lys Gln Leu Arg Ile Met  
 755 760 765  
 Gln Ser Ser Gln Ser Met Ser Lys Leu Thr Leu Thr Pro Trp Val Gly  
 770 775 780  
 Leu Arg Lys Ile Asn Val Ser Tyr Trp Cys Trp Glu Asp Met Ser Pro  
 785 790 795 800  
 Phe Thr Asn Ser Leu Gln Trp Met Pro Ser Glu Pro Ser Asp Ala  
 805 810 815  
 Gly Phe Cys Gly Ile Leu Ser Glu Pro Ser Thr Arg Gly Leu Lys Ala  
 820 825 830  
 Ala Thr Cys Ile Asn Pro Leu Asn Gly Ser Val Cys Glu Arg Pro Ala  
 835 840 845  
 Asn His Ser Ala Lys Gln Cys Arg Thr Pro Cys Ala Leu Arg Thr Ala  
 850 855 860  
 Cys Gly Asp Cys Thr Ser Gly Ser Ser Glu Cys Met Trp Cys Ser Asn  
 865 870 875 880  
 Met Lys Gln Cys Val Asp Ser Asn Ala Tyr Val Ala Ser Phe Pro Phe  
 885 890 895  
 Gly Gln Cys Met Glu Trp Tyr Thr Met Ser Thr Cys Pro Pro Glu Asn  
 900 905 910  
 Cys Ser Gly Tyr Cys Thr Cys Ser His Cys Leu Glu Gln Pro Gly Cys  
 915 920 925  
 Gly Trp Cys Thr Asp Pro Ser Asn Thr Gly Lys Gly Lys Cys Ile Glu  
 930 935 940  
 Gly Ser Tyr Lys Gly Pro Val Lys Met Pro Ser Gln Ala Pro Thr Gly  
 945 950 955 960  
 Asn Phe Tyr Pro Gln Pro Leu Leu Asn Ser Ser Met Cys Leu Glu Asp  
 965 970 975  
 Ser Arg Tyr Asn Trp Ser Phe Ile His Cys Pro Ala Cys Gln Cys Asn  
 980 985 990  
 Gly His Ser Lys Cys Ile Asn Gln Ser Ile Cys Glu Lys Cys Glu Asn  
 995 1000 1005  
 Leu Thr Thr Gly Lys His Cys Glu Thr Cys Ile Ser Gly Phe Tyr Gly  
 1010 1015 1020  
 Asp Pro Thr Asn Gly Gly Lys Cys Gln Pro Cys Lys Cys Asn Gly His  
 1025 1030 1035 1040  
 Ala Ser Leu Cys Asn Thr Asn Thr Gly Lys Cys Phe Cys Thr Thr Lys  
 1045 1050 1055

Gly Val Lys Gly Asp Glu Cys Gln Leu Cys Glu Val Glu Asn Arg Tyr  
 1060 1065 1070  
 Gln Gly Asn Pro Leu Arg Gly Thr Cys Tyr Tyr Thr Leu Leu Ile Asp  
 1075 1080 1085  
 Tyr Gln Phe Thr Phe Ser Leu Ser Gln Glu Asp Asp Arg Tyr Tyr Thr  
 1090 1095 1100  
 Ala Ile Asn Phe Val Ala Thr Pro Asp Glu Gln Asn Arg Asp Leu Asp  
 1105 1110 1115 1120  
 Met Phe Ile Asn Ala Ser Lys Asn Phe Asn Leu Asn Ile Thr Trp Ala  
 1125 1130 1135  
 Ala Ser Phe Ser Ala Gly Thr Gln Ala Gly Glu Glu Met Pro Val Val  
 1140 1145 1150  
 Ser Lys Thr Asn Ile Lys Glu Tyr Lys Asp Ser Phe Ser Asn Glu Lys  
 1155 1160 1165  
 Phe Asp Phe Arg Asn His Pro Asn Ile Thr Phe Phe Val Tyr Val Ser  
 1170 1175 1180  
 Asn Phe Thr Trp Pro Ile Lys Ile Gln Val Gln Thr Glu Gln  
 1185 1190 1195

<210> 3  
 <211> 34  
 <212> DNA  
 <213> Homo sapiens

<400> 3  
 cccaagcttg ggatgggtgt cgggctcagc ccgc

34

<210> 4  
 <211> 41  
 <212> DNA  
 <213> Homo sapiens

<400> 4  
 ataagaatgc ggcgctaaac tcattgttca gtttcgacct g

41

<210> 5  
 <211> 32  
 <212> DNA  
 <213> Homo sapiens

<400> 5  
 cccaagcttg ggatggtggc cgcagcggcg gc

32

<210> 6  
 <211> 25  
 <212> DNA  
 <213> Homo sapiens

<400> 6  
 ccaggtccat ctgtcacaaa cccag

25

<210> 7  
 <211> 38  
 <212> DNA  
 <213> Homo sapiens

<400> 7  
 gtgcgtgaag cttgtaccgg caactgaggc aaggctga

38

<210> 8  
 <211> 39  
 <212> DNA  
 <213> Homo sapiens

<400> 8  
 gtagtgttaa gtccacgttt gacttcgccg gcgtgcgtg

39



<210> 9  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated

<400> 9

Gly Ala Pro Val Pro Tyr Pro Asp Pro Leu Glu Pro Arg Ala Ala  
 1 5 10 15

<210> 10  
 <211> 1355  
 <212> PRT  
 <213> Homo sapiens

<400> 10

Met Val Ala Ala Ala Ala Thr Glu Ala Arg Leu Arg Arg Arg Thr  
 1 5 10 15  
 Ala Ala Thr Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Cys Val  
 20 25 30  
 Asn Gly Gly Arg Cys Asn Pro Gly Thr Gly Gln Cys Val Cys Pro Ala  
 35 40 45  
 Gly Trp Val Gly Glu Gln Cys Gln His Cys Gly Gly Arg Phe Arg Leu  
 50 55 60  
 Thr Gly Ser Ser Gly Phe Val Thr Asp Gly Pro Gly Asn Tyr Lys Tyr  
 65 70 75 80  
 Lys Thr Lys Cys Thr Trp Leu Ile Glu Gly Gln Pro Asn Arg Ile Met  
 85 90 95  
 Arg Leu Arg Phe Asn His Phe Ala Thr Glu Cys Ser Trp Asp His Leu  
 100 105 110  
 Tyr Val Tyr Asp Gly Asp Ser Ile Tyr Ala Pro Leu Val Ala Ala Phe  
 115 120 125  
 Ser Gly Leu Ile Val Pro Glu Arg Asp Gly Asn Glu Thr Val Pro Glu  
 130 135 140  
 Val Val Ala Thr Ser Gly Tyr Ala Leu Leu His Phe Phe Ser Asp Ala  
 145 150 155 160  
 Ala Tyr Asn Leu Thr Gly Phe Asn Ile Thr Tyr Ser Phe Asp Met Cys  
 165 170 175  
 Pro Asn Asn Cys Ser Gly Arg Gly Glu Cys Lys Ile Ser Asn Ser Ser  
 180 185 190  
 Asp Thr Val Glu Cys Glu Cys Ser Glu Asn Trp Lys Gly Glu Ala Cys  
 195 200 205  
 Asp Ile Pro His Cys Thr Asp Asn Cys Gly Phe Pro His Arg Gly Ile  
 210 215 220  
 Cys Asn Ser Ser Asp Val Arg Gly Cys Ser Cys Phe Ser Asp Trp Gln  
 225 230 235 240  
 Gly Pro Gly Cys Ser Val Pro Val Pro Ala Asn Gln Ser Phe Trp Thr  
 245 250 255  
 Arg Glu Glu Tyr Ser Asn Leu Lys Leu Pro Arg Ala Ser His Lys Ala  
 260 265 270  
 Val Val Asn Gly Asn Ile Met Trp Val Val Gly Gly Tyr Met Phe Asn  
 275 280 285  
 His Ser Asp Tyr Asn Met Val Leu Ala Tyr Asp Leu Ala Ser Arg Glu  
 290 295 300  
 Trp Leu Pro Leu Asn Arg Ser Val Asn Asn Val Val Val Arg Tyr Gly  
 305 310 315 320  
 His Ser Leu Ala Leu Tyr Lys Asp Lys Ile Tyr Met Tyr Gly Gly Lys  
 325 330 335  
 Ile Asp Ser Thr Gly Asn Val Thr Asn Glu Leu Arg Val Phe His Ile  
 340 345 350  
 His Asn Glu Ser Trp Val Leu Leu Thr Pro Lys Ala Lys Glu Gln Tyr  
 355 360 365  
 Ala Val Val Gly His Ser Ala His Ile Val Thr Leu Lys Asn Gly Arg  
 370 375 380

Val Val Met Leu Val Ile Phe Gly His Cys Pro Leu Tyr Gly Tyr Ile  
 385 390 395 400  
 Ser Asn Val Gln Glu Tyr Asp Leu Asp Lys Asn Thr Trp Ser Ile Leu  
 405 410 415  
 His Thr Gln Gly Ala Leu Val Gln Gly Gly Tyr Gly His Ser Ser Val  
 420 425 430  
 Tyr Asp His Arg Thr Arg Ala Leu Tyr Val His Gly Gly Tyr Lys Ala  
 435 440 445  
 Phe Ser Ala Asn Lys Tyr Arg Leu Ala Asp Asp Leu Tyr Arg Tyr Asp  
 450 455 460  
 Val Asp Thr Gln Met Trp Thr Ile Leu Lys Asp Ser Arg Phe Phe Arg  
 465 470 475 480  
 Tyr Leu His Thr Ala Val Ile Val Ser Gly Thr Met Leu Val Phe Gly  
 485 490 495  
 Gly Asn Thr His Asn Asp Thr Ser Met Ser His Gly Ala Lys Cys Phe  
 500 505 510  
 Ser Ser Asp Phe Met Ala Tyr Asp Ile Ala Cys Asp Arg Trp Ser Val  
 515 520 525  
 Leu Pro Arg Pro Asp Leu His His Asp Val Asn Arg Phe Gly His Ser  
 530 535 540  
 Ala Val Leu His Asn Ser Thr Met Tyr Val Phe Gly Gly Phe Asn Ser  
 545 550 555 560  
 Leu Leu Leu Ser Asp Ile Leu Val Phe Thr Ser Glu Gln Cys Asp Ala  
 565 570 575  
 His Arg Ser Glu Ala Ala Cys Leu Ala Ala Gly Pro Gly Ile Arg Cys  
 580 585 590  
 Val Trp Asn Thr Gly Ser Ser Gln Cys Ile Ser Trp Ala Leu Ala Thr  
 595 600 605  
 Asp Glu Gln Glu Glu Lys Leu Lys Ser Glu Cys Phe Ser Lys Arg Thr  
 610 615 620  
 Leu Asp His Asp Arg Cys Asp Gln His Thr Asp Cys Tyr Ser Cys Thr  
 625 630 635 640  
 Ala Asn Thr Asn Asp Cys His Trp Cys Asn Asp His Cys Val Pro Arg  
 645 650 655  
 Asn His Ser Cys Ser Glu Gly Gln Ile Ser Ile Phe Arg Tyr Glu Asn  
 660 665 670  
 Cys Pro Lys Asp Asn Pro Met Tyr Tyr Cys Asn Lys Lys Thr Ser Cys  
 675 680 685  
 Arg Ser Cys Ala Leu Asp Gln Asn Cys Gln Trp Glu Pro Arg Asn Gln  
 690 695 700  
 Glu Cys Ile Ala Leu Pro Glu Asn Ile Cys Gly Ile Gly Trp His Leu  
 705 710 715 720  
 Val Gly Asn Ser Cys Leu Lys Ile Thr Thr Ala Lys Glu Asn Tyr Asp  
 725 730 735  
 Asn Ala Lys Leu Phe Cys Arg Asn His Asn Ala Leu Leu Ala Ser Leu  
 740 745 750  
 Thr Thr Gln Lys Lys Val Glu Phe Val Leu Lys Gln Leu Arg Ile Met  
 755 760 765  
 Gln Ser Ser Gln Ser Met Ser Lys Leu Thr Leu Thr Pro Trp Val Gly  
 770 775 780  
 Leu Arg Lys Ile Asn Val Ser Tyr Trp Cys Trp Glu Asp Met Ser Pro  
 785 790 795 800  
 Phe Thr Asn Ser Leu Leu Gln Trp Met Pro Ser Glu Pro Ser Asp Ala  
 805 810 815  
 Gly Phe Cys Gly Ile Leu Ser Glu Pro Ser Thr Arg Gly Leu Lys Ala  
 820 825 830  
 Ala Thr Cys Ile Asn Pro Leu Asn Gly Ser Val Cys Glu Arg Pro Ala  
 835 840 845  
 Asn His Ser Ala Lys Gln Cys Arg Thr Pro Cys Ala Leu Arg Thr Ala  
 850 855 860  
 Cys Gly Asp Cys Thr Ser Gly Ser Ser Glu Cys Met Trp Cys Ser Asn  
 865 870 875 880  
 Met Lys Gln Cys Val Asp Ser Asn Ala Tyr Val Ala Ser Phe Pro Phe  
 885 890 895  
 Gly Gln Cys Met Glu Trp Tyr Thr Met Ser Thr Cys Pro Pro Glu Asn  
 900 905 910

Cys Ser Gly Tyr Cys Thr Cys Ser His Cys Leu Glu Gln Pro Gly Cys  
 915 920 925  
 Gly Trp Cys Thr Asp Pro Ser Asn Thr Gly Lys Gly Lys Cys Ile Glu  
 930 935 940  
 Gly Ser Tyr Lys Gly Pro Val Lys Met Pro Ser Gln Ala Pro Thr Gly  
 945 950 955 960  
 Asn Phe Tyr Pro Gln Pro Leu Leu Asn Ser Ser Met Cys Leu Glu Asp  
 965 970 975  
 Ser Arg Tyr Asn Trp Ser Phe Ile His Cys Pro Ala Cys Gln Cys Asn  
 980 985 990  
 Gly His Ser Lys Cys Ile Asn Gln Ser Ile Cys Glu Lys Cys Glu Asn  
 995 1000 1005  
 Leu Thr Thr Gly Lys His Cys Glu Thr Cys Ile Ser Gly Phe Tyr Gly  
 1010 1015 1020  
 Asp Pro Thr Asn Gly Gly Lys Cys Gln Pro Cys Lys Cys Asn Gly His  
 1025 1030 1035 1040  
 Ala Ser Leu Cys Asn Thr Asn Thr Gly Lys Cys Phe Cys Thr Thr Lys  
 1045 1050 1055  
 Gly Val Lys Gly Asp Glu Cys Gln Leu Cys Glu Val Glu Asn Arg Tyr  
 1060 1065 1070  
 Gln Gly Asn Pro Leu Arg Gly Thr Cys Tyr Tyr Thr Leu Leu Ile Asp  
 1075 1080 1085  
 Tyr Gln Phe Thr Phe Ser Leu Ser Gln Glu Asp Asp Arg Tyr Tyr Thr  
 1090 1095 1100  
 Ala Ile Asn Phe Val Ala Thr Pro Asp Glu Gln Asn Arg Asp Leu Asp  
 1105 1110 1115 1120  
 Met Phe Ile Asn Ala Ser Lys Asn Phe Asn Leu Asn Ile Thr Trp Ala  
 1125 1130 1135  
 Ala Ser Phe Ser Ala Gly Thr Gln Ala Gly Glu Glu Met Pro Val Val  
 1140 1145 1150  
 Ser Lys Thr Asn Ile Lys Glu Tyr Lys Asp Ser Phe Ser Asn Glu Lys  
 1155 1160 1165  
 Phe Asp Phe Arg Asn His Pro Asn Ile Thr Phe Phe Val Tyr Val Ser  
 1170 1175 1180  
 Asn Phe Thr Trp Pro Ile Lys Ile Gln Ile Ala Phe Ser Gln His Ser  
 1185 1190 1195 1200  
 Asn Phe Met Asp Leu Val Gln Phe Phe Val Thr Phe Phe Ser Cys Phe  
 1205 1210 1215  
 Leu Ser Leu Leu Val Ala Ala Val Val Trp Lys Ile Lys Gln Ser  
 1220 1225 1230  
 Cys Trp Ala Ser Arg Arg Arg Glu Gln Leu Leu Arg Glu Met Gln Gln  
 1235 1240 1245  
 Met Ala Ser Arg Pro Phe Ala Ser Val Asn Val Ala Leu Glu Thr Asp  
 1250 1255 1260  
 Glu Glu Pro Pro Asp Leu Ile Gly Gly Ser Ile Lys Thr Val Pro Lys  
 1265 1270 1275 1280  
 Pro Ile Ala Leu Glu Pro Cys Phe Gly Asn Lys Ala Ala Val Leu Ser  
 1285 1290 1295  
 Val Phe Val Arg Leu Pro Arg Gly Leu Gly Gly Ile Pro Pro Gly  
 1300 1305 1310  
 Gln Ser Gly Leu Ala Val Ala Ser Ala Leu Val Asp Ile Ser Gln Gln  
 1315 1320 1325  
 Met Pro Ile Val Tyr Lys Glu Lys Ser Gly Ala Val Arg Asn Arg Lys  
 1330 1335 1340  
 Gln Gln Pro Pro Ala Gln Pro Gly Thr Cys Ile  
 1345 1350 1355

<210> 11  
 <211> 4068  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(4065)

<400> 11

atg gtg gcc gca gcg gcg gca act gag gca agg ctg agg agg agg acg	48
Met Val Ala Ala Ala Ala Thr Glu Ala Arg Leu Arg Arg Arg Thr	
1 5 10 15	
gcg gcg acg gca gcg ctc gcg ggc agg agc ggc ggg ccg cac tgt gtc	96
Ala Ala Thr Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Cys Val	
20 25 30	
aac ggc ggt cgc tgc aac cct ggc acc ggc cag tgc gtc tgc ccc gcc	144
Asn Gly Gly Arg Cys Asn Pro Gly Thr Gly Gln Cys Val Cys Pro Ala	
35 40 45	
ggc tgg gtg ggc gag caa tgc cag cac tgc ggg ggc cgc ttc aga cta	192
Gly Trp Val Gly Glu Gln Cys Gln His Cys Gly Gly Arg Phe Arg Leu	
50 55 60	
act gga tct tct ggg ttt gtg aca gat gga cct gga aat tat aaa tac	240
Thr Gly Ser Ser Gly Phe Val Thr Asp Gly Pro Gly Asn Tyr Lys Tyr	
65 70 75 80	
aaa acg aag tgc acg tgg ctc att gaa gga cag cca aat aga ata atg	288
Lys Thr Lys Cys Thr Trp Leu Ile Glu Gly Gln Pro Asn Arg Ile Met	
85 90 95	
aga ctt cgt ttc aat cat ttt gct aca gag tgt agt tgg gac cat tta	336
Arg Leu Arg Phe Asn His Phe Ala Thr Glu Cys Ser Trp Asp His Leu	
100 105 110	
tat gtt tat gat ggg gac tca att tat gca ccg cta gtt gct gca ttt	384
Tyr Val Tyr Asp Gly Asp Ser Ile Tyr Ala Pro Leu Val Ala Ala Phe	
115 120 125	
agt ggc ctc att gtt cct gag aga gat ggc aat gag act gtc cct gag	432
Ser Gly Leu Ile Val Pro Glu Arg Asp Gly Asn Glu Thr Val Pro Glu	
130 135 140	
ggt gtt gcc aca tca ggt tat gcc ttg ctg cat ttt ttt agt gat gct	480
Val Val Ala Thr Ser Gly Tyr Ala Leu Leu His Phe Phe Ser Asp Ala	
145 150 155 160	
gct tat aat ttg act gga ttt aat att act tac agt ttt gat atg tgt	528
Ala Tyr Asn Leu Thr Gly Phe Asn Ile Thr Tyr Ser Phe Asp Met Cys	
165 170 175	
cca aat aac tgc tca ggc cga gga gag tgt aag atc agt aat agc agc	576
Pro Asn Asn Cys Ser Gly Arg Gly Glu Cys Lys Ile Ser Asn Ser Ser	
180 185 190	
gat act gtt gaa tgt gaa tgt tct gaa aac tgg aaa ggt gaa gca tgt	624
Asp Thr Val Glu Cys Glu Cys Ser Glu Asn Trp Lys Gly Glu Ala Cys	
195 200 205	
gac att cct cac tgt aca gac aac tgt ggt ttt cct cat cga ggc atc	672
Asp Ile Pro His Cys Thr Asp Asn Cys Gly Phe Pro His Arg Gly Ile	
210 215 220	
tgc aat tca agt gat gtc aga gga tgc tcc tgc ttc tca gac tgg cag	720
Cys Asn Ser Ser Asp Val Arg Gly Cys Ser Cys Phe Ser Asp Trp Gln	
225 230 235 240	
ggt cct gga tgt tca gtt cct gta cca gct aac cag tca ttt tgg act	768
Gly Pro Gly Cys Ser Val Pro Val Pro Ala Asn Gln Ser Phe Trp Thr	
245 250 255	

cga gag gaa tat tct aac tta aag ctc ccc aga gca tct cat aaa gct Arg Glu Glu Tyr Ser Asn Leu Lys Leu Pro Arg Ala Ser His Lys Ala 260 265 270	816
gtg gtc aat gga aac att atg tgg gtt gtt gga gga tat atg ttc aac Val Val Asn Gly Asn Ile Met Trp Val Val Gly Gly Tyr Met Phe Asn 275 280 285	864
cac tca gat tat aac atg gtt cta gcg tat gac ctt gct tct agg gag His Ser Asp Tyr Asn Met Val Leu Ala Tyr Asp Leu Ala Ser Arg Glu 290 295 300	912
tgg ctt cca cta aac cgt tct gtg aac aat gtg gtt gtt aga tat ggt Trp Leu Pro Leu Asn Arg Ser Val Asn Asn Val Val Arg Tyr Gly 305 310 315 320	960
cat tct ttg gca tta tac aag gat aaa att tac atg tat gga gga aaa His Ser Leu Ala Leu Tyr Lys Asp Lys Ile Tyr Met Tyr Gly Gly Lys 325 330 335	1008
att gat tca act ggg aat gtg acc aat gag ttg aga gtt ttt cac att Ile Asp Ser Thr Gly Asn Val Thr Asn Glu Leu Arg Val Phe His Ile 340 345 350	1056
cat aat gag tca tgg gtg ttg ttg acc cct aag gca aag gag cag tat His Asn Glu Ser Trp Val Leu Leu Thr Pro Lys Ala Lys Glu Gln Tyr 355 360 365	1104
gca gtg gtt ggg cac tct gca cac att gtt aca ctg aag aat ggc cga Ala Val Val Gly His Ser Ala His Ile Val Thr Leu Lys Asn Gly Arg 370 375 380	1152
gtg gtc atg ctg gtc atc ttt ggt cac tgc cct ctc tat gga tat ata Val Val Met Leu Val Ile Phe Gly His Cys Pro Leu Tyr Gly Tyr Ile 385 390 395 400	1200
agc aat gtg cag gaa tat gat ttg gat aag aac aca tgg agt ata tta Ser Asn Val Gln Glu Tyr Asp Leu Asp Lys Asn Thr Trp Ser Ile Leu 405 410 415	1248
cac acc cag ggt gcc ctt gtg caa ggg ggt tac ggc cat agc agt gtt His Thr Gln Gly Ala Leu Val Gln Gly Gly Tyr Gly His Ser Ser Val 420 425 430	1296
tac gac cat agg acc agg gcc cta tac gtt cat ggt ggc tac aag gct Tyr Asp His Arg Thr Arg Ala Leu Tyr Val His Gly Gly Tyr Lys Ala 435 440 445	1344
ttc agt gcc aat aag tac cgg ctt gca gat gat ctc tac cga tat gat Phe Ser Ala Asn Lys Tyr Arg Leu Ala Asp Asp Leu Tyr Arg Tyr Asp 450 455 460	1392
gtg gat acc cag atg tgg acc att ctt aag gac agc cga ttt ttc cgt Val Asp Thr Gln Met Trp Thr Ile Leu Lys Asp Ser Arg Phe Phe Arg 465 470 475 480	1440
tac ttg cac aca gct gtg ata gtg agt gga acc atg ctg gtg ttt ggg Tyr Leu His Thr Ala Val Ile Val Ser Gly Thr Met Leu Val Phe Gly 485 490 495	1488
gga aac aca cac aat gac aca tct atg agc cat ggc gcc aaa tgc ttc Gly Asn Thr His Asn Asp Thr Ser Met Ser His Gly Ala Lys Cys Phe 500 505 510	1536
tct tca gat ttc atg gcc tat gac att gcc tgt gac cgc tgg tca gtg Ser Ser Asp Phe Met Ala Tyr Asp Ile Ala Cys Asp Arg Trp Ser Val 515 520 525	1584

ctt ccc aga cct gat ctc cac cat gat gtc aac aga ttt ggc cat tca Leu Pro Arg Pro Asp Leu His His Asp Val Asn Arg Phe Gly His Ser 530 535 540	1632
gca gtc tta cac aac agc acc atg tat gtg ttc ggt ggt ttc aat agt Ala Val Leu His Asn Ser Thr Met Tyr Val Phe Gly Gly Phe Asn Ser 545 550 555 560	1680
ctc ctc ctc agc gac atc ctg gta ttc acc tcg gaa cag tgt gat gcg Leu Leu Leu Ser Asp Ile Leu Val Phe Thr Ser Glu Gln Cys Asp Ala 565 570 575	1728
cat cgg agt gaa gcc gct tgt tta gca gca gga cct ggt att cgg tgt His Arg Ser Glu Ala Ala Cys Leu Ala Ala Gly Pro Gly Ile Arg Cys 580 585 590	1776
gtg tgg aac aca ggg tcg tct cag tgt atc tcg tgg gcg ctg gca act Val Trp Asn Thr Gly Ser Ser Gln Cys Ile Ser Trp Ala Leu Ala Thr 595 600 605	1824
gat gaa caa gaa gaa aag tta aaa tca gaa tgt ttt tcc aaa aga act Asp Glu Gln Glu Lys Leu Lys Ser Glu Cys Phe Ser Lys Arg Thr 610 615 620	1872
ctt gac cat gac aga tgt gac cag cac aca gat tgt tac agc tgc aca Leu Asp His Asp Arg Cys Asp Gln His Thr Asp Cys Tyr Ser Cys Thr 625 630 635 640	1920
gcc aac acc aat gac tgc cac tgg tgc aat gac cat tgt gtc ccc agg Ala Asn Thr Asn Asp Cys His Trp Cys Asn Asp His Cys Val Pro Arg 645 650 655	1968
aac cac agc tgc tca gaa ggc cag atc tcc att ttt agg tat gag aat Asn His Ser Cys Ser Glu Gly Gln Ile Ser Ile Phe Arg Tyr Glu Asn 660 665 670	2016
tgc ccc aag gat aac cct atg tac tac tgt aac aag aag acc agc tgc Cys Pro Lys Asp Asn Pro Met Tyr Tyr Cys Asn Lys Lys Thr Ser Cys 675 680 685	2064
agg agc tgt gcc ctg gac cag aac tgc cag tgg gag ccc cgg aat cag Arg Ser Cys Ala Leu Asp Gln Asn Cys Gln Trp Glu Pro Arg Asn Gln 690 695 700	2112
gag tgc att gcc ctg ccc gaa aat atc tgt ggc att ggc tgg cat ttg Glu Cys Ile Ala Leu Pro Glu Asn Ile Cys Gly Ile Gly Trp His Leu 705 710 715 720	2160
gtt gga aac tca tgt ttg aaa att act act gcc aag gag aat tat gac Val Gly Asn Ser Cys Leu Lys Ile Thr Thr Ala Lys Glu Asn Tyr Asp 725 730 735	2208
aat gct aaa ttg ttc tgt agg aac cac aat gcc ctt ttg gct tct ctt Asn Ala Lys Leu Phe Cys Arg Asn His Asn Ala Leu Leu Ala Ser Leu 740 745 750	2256
aca acc cag aag aag gta gaa ttt gtc ctt aag cag ctg cga ata atg Thr Thr Gln Lys Lys Val Glu Phe Val Leu Lys Gln Arg Ile Met 755 760 765	2304
cag tca tct cag agc atg tcc aag ctc acc tta acc cca tgg gtc ggc Gln Ser Ser Gln Ser Met Ser Lys Leu Thr Leu Pro Trp Val Gly 770 775 780	2352

ctt cgg aag atc aat gtg tcc tac tgg tgc tgg gaa gat atg tcc cca Leu Arg Lys Ile Asn Val Ser Tyr Trp Cys Trp Glu Asp Met Ser Pro 785 790 795 800	2400
ttt aca aat agt tta cta cag tgg atg ccg tct gag ccc agt gat gct Phe Thr Asn Ser Leu Leu Gln Trp Met Pro Ser Glu Pro Ser Asp Ala 805 810 815	2448
gga ttc tgt gga att tta tca gaa ccc agt act cgg gga ctg aag gct Gly Phe Cys Gly Ile Leu Ser Glu Pro Ser Thr Arg Gly Leu Lys Ala 820 825 830	2496
gca acc tgc atc aac cca ctc aat ggt agt gtc tgt gaa agg cct gca Ala Thr Cys Ile Asn Pro Leu Asn Gly Ser Val Cys Glu Arg Pro Ala 835 840 845	2544
aac cac agt gct aag cag tgc cgg aca cca tgt gcc ttg agg aca gca Asn His Ser Ala Lys Gln Cys Arg Thr Pro Cys Ala Leu Arg Thr Ala 850 855 860	2592
tgt gga gat tgc acc agc ggc agc tct gag tgc atg tgg tgc agc aac Cys Gly Asp Cys Thr Ser Gly Ser Ser Glu Cys Met Trp Cys Ser Asn 865 870 875 880	2640
atg aag cag tgt gtg gac tcc aat gcc tat gtg gcc tcc ttc cct ttt Met Lys Gln Cys Val Asp Ser Asn Ala Tyr Val Ala Ser Phe Pro Phe 885 890 895	2688
ggc cag tgt atg gaa tgg tat acg atg agc acc tgc ccc cct gaa aat Gly Gln Cys Met Glu Trp Tyr Thr Met Ser Thr Cys Pro Pro Glu Asn 900 905 910	2736
tgt tca ggc tac tgt acc tgt agt cat tgc ttg gag caa cca ggc tgt Cys Ser Gly Tyr Cys Thr Cys Ser His Cys Leu Glu Gln Pro Gly Cys 915 920 925	2784
ggc tgg tgt act gat ccc agc aat act ggc aaa ggg aaa tgc ata gag Gly Trp Cys Thr Asp Pro Ser Asn Thr Gly Lys Gly Lys Cys Ile Glu 930 935 940	2832
ggt tcc tat aaa gga cca gtg aag atg cct tgc caa gcc cct aca gga Gly Ser Tyr Lys Gly Pro Val Lys Met Pro Ser Gln Ala Pro Thr Gly 945 950 955 960	2880
aat ttc tat cca cag ccc ctg ctc aat tcc agc atg tgt cta gag gac Asn Phe Tyr Pro Gln Pro Leu Leu Asn Ser Ser Met Cys Leu Glu Asp 965 970 975	2928
agc aga tac aac tgg tct ttc att cac tgt cca gct tgc caa tgc aac Ser Arg Tyr Asn Trp Ser Phe Ile His Cys Pro Ala Cys Gln Cys Asn 980 985 990	2976
ggc cac agt aaa tgc atc aat cag agc atc tgt gag aag tgt gag aac Gly His Ser Lys Cys Ile Asn Gln Ser Ile Cys Glu Lys Cys Glu Asn 995 1000 1005	3024
ctg acc aca ggc aag cac tgc gag acc tgc ata tct ggc ttc tac ggt Leu Thr Thr Gly Lys His Cys Glu Thr Cys Ile Ser Gly Phe Tyr Gly 1010 1015 1020	3072
gat ccc acc aat gga ggg aaa tgt cag cca tgc aag tgc aat ggg cac Asp Pro Thr Asn Gly Gly Lys Cys Gln Pro Cys Lys Cys Asn Gly His 1025 1030 1035 1040	3120
gcg tct ctg tgc aac acc aac acg ggc aag tgc ttc tgc acc acc aag Ala Ser Leu Cys Asn Thr Asn Thr Gly Lys Cys Phe Cys Thr Thr Lys 1045 1050 1055	3168

ggc gtc aag ggg gac gag tgc cag cta tgt gag gta gaa aat cga tac Gly Val Lys Gly Asp Glu Cys Gln Leu Cys Glu Val Glu Asn Arg Tyr 1060 1065 1070	3216
caa gga aac cct ctc aga gga aca tgt tat tat act ctt ctt att gac Gln Gly Asn Pro Leu Arg Gly Thr Cys Tyr Tyr Thr Leu Leu Ile Asp 1075 1080 1085	3264
tat cag ttc acc ttt agt cta tcc cag gaa gat gat cgc tat tac aca Tyr Gln Phe Thr Phe Ser Leu Ser Gln Glu Asp Asp Arg Tyr Tyr Thr 1090 1095 1100	3312
gct atc aat ttt gtg gct act cct gac gaa caa aac agg gat ttg gac Ala Ile Asn Phe Val Ala Thr Pro Asp Glu Gln Asn Arg Asp Leu Asp 1105 1110 1115 1120	3360
atg ttc atc aat gcc tcc aag aat ttc aac ctc aac atc acc tgg gct Met Phe Ile Asn Ala Ser Lys Asn Phe Asn Leu Asn Ile Thr Trp Ala 1125 1130 1135	3408
gcc agt ttc tca gct gga acc cag gct gga gaa gag atg cct gtt gtt Ala Ser Phe Ser Ala Gly Thr Gln Ala Gly Glu Glu Met Pro Val Val 1140 1145 1150	3456
tca aaa acc aac att aag gag tac aaa gat agt ttc tct aat gag aag Ser Lys Thr Asn Ile Lys Glu Tyr Lys Asp Ser Phe Ser Asn Glu Lys 1155 1160 1165	3504
ttt gat ttt cgc aac cac cca aat atc act ttc ttt gtt tat gtc agt Phe Asp Phe Arg Asn His Pro Asn Ile Thr Phe Phe Val Tyr Val Ser 1170 1175 1180	3552
aat ttc acc tgg ccc atc aaa att cag att gcc ttc tct cag cac agc Asn Phe Thr Trp Pro Ile Lys Ile Gln Ile Ala Phe Ser Gln His Ser 1185 1190 1195 1200	3600
aat ttt atg gac ctg gta cag ttc ttc gtg act ttc ttc agt tgt ttc Asn Phe Met Asp Leu Val Gln Phe Phe Val Thr Phe Phe Ser Cys Phe 1205 1210 1215	3648
ctc tct ttg ctc ctg gtg gct gct gtg gtt tgg aag atc aaa caa agt Leu Ser Leu Leu Leu Val Ala Ala Val Val Trp Lys Ile Lys Gln Ser 1220 1225 1230	3696
tgt tgg gcc tcc aga cgt aga gag caa ctt ctt cga gag atg caa cag Cys Trp Ala Ser Arg Arg Arg Glu Gln Leu Leu Arg Glu Met Gln Gln 1235 1240 1245	3744
atg gcc agc cgt ccc ttt gcc tct gta aat gtc gcc ttg gaa aca gat Met Ala Ser Arg Pro Phe Ala Ser Val Asn Val Ala Leu Glu Thr Asp 1250 1255 1260	3792
gag gag cct cct gat ctt att ggg ggg agt ata aag act gtt ccc aaa Glu Glu Pro Pro Asp Leu Ile Gly Gly Ser Ile Lys Thr Val Pro Lys 1265 1270 1275 1280	3840
ccc att gca ctg gag ccg tgt ttt ggc aac aaa gcc gct gtc ctc tct Pro Ile Ala Leu Glu Pro Cys Phe Gly Asn Lys Ala Ala Val Leu Ser 1285 1290 1295	3888
gtg ttt gtg agg ctc cct cga ggc ctg ggt ggc atc cct cct cct ggg Val Phe Val Arg Leu Pro Arg Gly Leu Gly Gly Ile Pro Pro Pro Gly 1300 1305 1310	3936
cag tca ggt ctt gct gtg gcc agc gcc ctg gtg gac att tct cag cag Gln Ser Gly Leu Ala Val Ala Ser Ala Leu Val Asp Ile Ser Gln Gln	3984



1315 1320 1325  
 atg ccg ata gtg tac aag gag aag tca gga gcc gtg aga aac cgg aag 4032  
 Met Pro Ile Val Tyr Lys Glu Lys Ser Gly Ala Val Arg Asn Arg Lys  
 1330 1335 1340

cag cag ccc cct gca cag cct ggg acc tgc atc tga 4068  
 Gln Gln Pro Pro Ala Gln Pro Gly Thr Cys Ile  
 1345 1350 1355

<210> 12  
 <211> 1429  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
 Met Val Ala Ala Ala Ala Thr Glu Ala Arg Leu Arg Arg Arg Thr  
 1 5 10 15  
 Ala Ala Thr Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Trp Asp  
 20 25 30  
 Trp Asp Val Thr Arg Ala Gly Arg Pro Gly Leu Gly Ala Gly Leu Arg  
 35 40 45  
 Leu Pro Arg Leu Leu Ser Pro Pro Leu Arg Pro Arg Leu Leu Leu  
 50 55 60  
 Leu Leu Leu Leu Pro Pro Leu Leu Leu Leu Leu Pro Cys Glu  
 65 70 75 80  
 Ala Glu Ala Ala Ala Ala Ala Ala Val Ser Gly Ser Ala Ala Ala  
 85 90 95  
 Glu Ala Lys Glu Cys Asp Arg Pro Cys Val Asn Gly Gly Arg Cys Asn  
 100 105 110  
 Pro Gly Thr Gly Gln Cys Val Cys Pro Ala Gly Trp Val Gly Glu Gln  
 115 120 125  
 Cys Gln His Cys Gly Gly Arg Phe Arg Leu Thr Gly Ser Ser Gly Phe  
 130 135 140  
 Val Thr Asp Gly Pro Gly Asn Tyr Lys Tyr Lys Thr Lys Cys Thr Trp  
 145 150 155 160  
 Leu Ile Glu Gly Gln Pro Asn Arg Ile Met Arg Leu Arg Phe Asn His  
 165 170 175  
 Phe Ala Thr Glu Cys Ser Trp Asp His Leu Tyr Val Tyr Asp Gly Asp  
 180 185 190  
 Ser Ile Tyr Ala Pro Leu Val Ala Ala Phe Ser Gly Leu Ile Val Pro  
 195 200 205  
 Glu Arg Asp Gly Asn Glu Thr Val Pro Glu Val Val Ala Thr Ser Gly  
 210 215 220  
 Tyr Ala Leu Leu His Phe Phe Ser Asp Ala Ala Tyr Asn Leu Thr Gly  
 225 230 235 240  
 Phe Asn Ile Thr Tyr Ser Phe Asp Met Cys Pro Asn Asn Cys Ser Gly  
 245 250 255  
 Arg Gly Glu Cys Lys Ile Ser Asn Ser Ser Glu Thr Val Glu Cys Glu  
 260 265 270  
 Cys Ser Glu Asn Trp Lys Gly Glu Ala Cys Asp Ile Pro His Cys Thr  
 275 280 285  
 Asp Asn Cys Gly Phe Pro His Arg Gly Ile Cys Asn Ser Ser Asp Val  
 290 295 300  
 Arg Gly Cys Ser Cys Phe Ser Asp Trp Gln Gly Pro Gly Cys Ser Val  
 305 310 315 320  
 Pro Val Pro Ala Asn Gln Ser Phe Trp Thr Arg Glu Glu Tyr Ser Asn  
 325 330 335  
 Leu Lys Leu Pro Arg Ala Ser His Lys Ala Val Val Asn Gly Asn Ile  
 340 345 350  
 Met Trp Val Val Gly Gly Tyr Met Phe Asn His Ser Asp Tyr Asn Met  
 355 360 365  
 Val Leu Ala Tyr Asp Leu Ala Ser Arg Glu Trp Leu Pro Leu Asn Arg  
 370 375 380  
 Ser Val Asn Asn Val Val Val Arg Tyr Gly His Ser Leu Ala Leu Tyr  
 385 390 395 400

Lys Asp Lys Ile Tyr Met Tyr Gly Gly Lys Ile Asp Pro Thr Gly Asn  
 405 410 415  
 Val Thr Asn Glu Leu Arg Val Phe His Ile His Asn Glu Ser Trp Val  
 420 425 430  
 Leu Leu Thr Pro Lys Ala Lys Glu Gln Tyr Ala Val Val Gly His Ser  
 435 440 445  
 Ala His Ile Val Thr Leu Lys Asn Gly Arg Val Val Met Leu Val Ile  
 450 455 460  
 Phe Gly His Cys Pro Leu Tyr Gly Tyr Ile Ser Asn Val Gln Glu Tyr  
 465 470 475 480  
 Asp Leu Asp Lys Asn Thr Trp Ser Ile Leu His Thr Gln Gly Ala Leu  
 485 490 495  
 Val Gln Gly Gly Tyr Gly His Ser Ser Val Tyr Asp His Arg Thr Arg  
 500 505 510  
 Ala Leu Tyr Val His Gly Gly Tyr Lys Ala Phe Ser Ala Asn Lys Tyr  
 515 520 525  
 Arg Leu Ala Asp Asp Leu Tyr Arg Tyr Asp Val Asp Thr Gln Met Trp  
 530 535 540  
 Thr Ile Leu Lys Asp Ser Arg Phe Phe Arg Tyr Leu His Thr Ala Val  
 545 550 555 560  
 Ile Val Ser Gly Thr Met Leu Val Phe Gly Gly Asn Thr His Asn Asp  
 565 570 575  
 Thr Ser Met Ser His Gly Ala Lys Cys Phe Ser Ser Asp Phe Met Ala  
 580 585 590  
 Tyr Asp Ile Ala Cys Asp Arg Trp Ser Val Leu Pro Arg Pro Asp Leu  
 595 600 605  
 His His Asp Val Asn Arg Phe Gly His Ser Ala Val Leu His Asn Ser  
 610 615 620  
 Thr Met Tyr Val Phe Gly Gly Phe Asn Ser Leu Leu Ser Asp Ile  
 625 630 635 640  
 Leu Val Phe Thr Ser Glu Gln Cys Asp Ala His Arg Ser Glu Ala Ala  
 645 650 655  
 Cys Leu Ala Ala Gly Pro Gly Ile Arg Cys Val Trp Asn Thr Gly Ser  
 660 665 670  
 Ser Gln Cys Ile Ser Trp Ala Leu Ala Thr Asp Glu Gln Glu Glu Lys  
 675 680 685  
 Leu Lys Ser Glu Cys Phe Ser Lys Arg Thr Leu Asp His Asp Arg Cys  
 690 695 700  
 Asp Gln His Thr Asp Cys Tyr Ser Cys Thr Ala Asn Thr Asn Asp Cys  
 705 710 715 720  
 His Trp Cys Asn Asp His Cys Val Pro Arg Asn His Ser Cys Ser Glu  
 725 730 735  
 Gly Gln Ile Ser Ile Phe Arg Tyr Glu Asn Cys Pro Lys Asp Asn Pro  
 740 745 750  
 Met Tyr Tyr Cys Asn Lys Lys Thr Ser Cys Arg Ser Cys Ala Leu Asp  
 755 760 765  
 Gln Asn Cys Gln Trp Glu Pro Arg Asn Gln Glu Cys Ile Ala Leu Pro  
 770 775 780  
 Glu Asn Ile Cys Gly Ile Gly Trp His Leu Val Gly Asn Ser Cys Leu  
 785 790 795 800  
 Lys Ile Thr Thr Ala Lys Glu Asn Tyr Asp Asn Ala Lys Leu Phe Cys  
 805 810 815  
 Arg Asn His Asn Ala Leu Leu Ala Ser Leu Thr Thr Gln Lys Lys Val  
 820 825 830  
 Glu Phe Val Leu Lys Gln Leu Arg Ile Met Gln Ser Ser Gln Ser Met  
 835 840 845  
 Ser Lys Leu Thr Leu Thr Pro Trp Val Gly Leu Arg Lys Ile Asn Val  
 850 855 860  
 Ser Tyr Trp Cys Trp Glu Asp Met Ser Pro Phe Thr Asn Ser Leu Leu  
 865 870 875 880  
 Gln Trp Met Pro Ser Glu Pro Ser Asp Ala Gly Phe Cys Gly Ile Leu  
 885 890 895  
 Ser Glu Pro Ser Thr Arg Gly Leu Lys Ala Ala Thr Cys Ile Asn Pro  
 900 905 910  
 Leu Asn Gly Ser Val Cys Glu Arg Pro Ala Asn His Ser Ala Lys Gln  
 915 920 925

Cys Arg Thr Pro Cys Ala Leu Arg Thr Ala Cys Gly Asp Cys Thr Ser  
 930 935 940  
 Gly Ser Ser Glu Cys Met Trp Cys Ser Asn Met Lys Gln Cys Val Asp  
 945 950 955 960  
 Ser Asn Ala Tyr Val Ala Ser Phe Pro Phe Gly Gln Cys Met Glu Trp  
 965 970 975  
 Tyr Thr Met Ser Thr Cys Pro Pro Glu Asn Cys Ser Gly Tyr Cys Thr  
 980 985 990  
 Cys Ser His Cys Leu Glu Gln Pro Gly Cys Gly Trp Cys Thr Asp Pro  
 995 1000 1005  
 Ser Asn Thr Gly Lys Gly Lys Cys Ile Glu Gly Ser Tyr Lys Gly Pro  
 1010 1015 1020  
 Val Lys Met Pro Ser Gln Ala Pro Thr Gly Asn Phe Tyr Pro Gln Pro  
 1025 1030 1035 1040  
 Leu Leu Asn Ser Ser Met Cys Leu Glu Asp Ser Arg Tyr Asn Trp Ser  
 1045 1050 1055  
 Phe Ile His Cys Pro Ala Cys Gln Cys Asn Gly His Ser Lys Cys Ile  
 1060 1065 1070  
 Asn Gln Ser Ile Cys Glu Lys Cys Glu Asn Leu Thr Thr Gly Lys His  
 1075 1080 1085  
 Cys Glu Thr Cys Ile Ser Gly Phe Tyr Gly Asp Pro Thr Asn Gly Gly  
 1090 1095 1100  
 Lys Cys Gln Pro Cys Lys Cys Asn Gly His Ala Ser Leu Cys Asn Thr  
 1105 1110 1115 1120  
 Asn Thr Gly Lys Cys Phe Cys Thr Thr Lys Gly Val Lys Gly Asp Glu  
 1125 1130 1135  
 Cys Gln Leu Cys Glu Val Glu Asn Arg Tyr Gln Gly Asn Pro Leu Arg  
 1140 1145 1150  
 Gly Thr Cys Tyr Tyr Thr Leu Leu Ile Asp Tyr Gln Phe Thr Phe Ser  
 1155 1160 1165  
 Leu Ser Gln Glu Asp Asp Arg Tyr Tyr Thr Ala Ile Asn Phe Val Ala  
 1170 1175 1180  
 Thr Pro Asp Glu Gln Asn Arg Asp Leu Asp Met Phe Ile Asn Ala Ser  
 1185 1190 1195 1200  
 Lys Asn Phe Asn Leu Asn Ile Thr Trp Ala Ala Ser Phe Ser Ala Gly  
 1205 1210 1215  
 Thr Gln Ala Gly Glu Glu Met Pro Val Val Ser Lys Thr Asn Ile Lys  
 1220 1225 1230  
 Glu Tyr Lys Asp Ser Phe Ser Asn Glu Lys Phe Asp Phe Arg Asn His  
 1235 1240 1245  
 Pro Asn Ile Thr Phe Phe Val Tyr Val Ser Asn Phe Thr Trp Pro Ile  
 1250 1255 1260  
 Lys Ile Gln Ile Ala Phe Ser Gln His Ser Asn Phe Met Asp Leu Val  
 1265 1270 1275 1280  
 Gln Phe Phe Val Thr Phe Phe Ser Cys Phe Leu Ser Leu Leu Val  
 1285 1290 1295  
 Ala Ala Val Val Trp Lys Ile Lys Gln Ser Cys Trp Ala Ser Arg Arg  
 1300 1305 1310  
 Arg Glu Gln Leu Leu Arg Glu Met Gln Gln Met Ala Ser Arg Pro Phe  
 1315 1320 1325  
 Ala Ser Val Asn Val Ala Leu Glu Thr Asp Glu Glu Pro Pro Asp Leu  
 1330 1335 1340  
 Ile Gly Gly Ser Ile Lys Thr Val Pro Lys Pro Ile Ala Leu Glu Pro  
 1345 1350 1355 1360  
 Cys Phe Gly Asn Lys Ala Ala Val Leu Ser Val Phe Val Arg Leu Pro  
 1365 1370 1375  
 Arg Gly Leu Gly Gly Ile Pro Pro Pro Gly Gln Ser Gly Leu Ala Val  
 1380 1385 1390  
 Ala Ser Ala Leu Val Asp Ile Ser Gln Gln Met Pro Ile Val Tyr Lys  
 1395 1400 1405  
 Glu Lys Ser Gly Ala Val Arg Asn Arg Lys Gln Gln Pro Pro Ala Gln  
 1410 1415 1420  
 Pro Gly Thr Cys Ile  
 1425

&lt;210&gt; 13

&lt;211&gt; 4290

<212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(4287)

<400> 13

atg gtg gcc gca gcg gcg gca act gag gca agg ctg agg agg agg acg	48
Met Val Ala Ala Ala Ala Ala Thr Glu Ala Arg Leu Arg Arg Arg Thr	
1 5 10 15	
gcg gcg acg gca gcg ctc gcg ggc agg agc ggc ggg ccg cac tgg gac	96
Ala Ala Thr Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Trp Asp	
20 25 30	
tgg gac gtg acc agg gct ggg agg ccg ggg ctg ggg gcc ggg ctg cgc	144
Trp Asp Val Thr Arg Ala Gly Arg Pro Gly Leu Gly Ala Gly Leu Arg	
35 40 45	
ctc ccg ccg ctg ctg tct cca ccg ctg ccg cca ccg ctg ctg ctg ctg	192
Leu Pro Arg Leu Leu Ser Pro Pro Leu Arg Pro Arg Leu Leu Leu Leu	
50 55 60	
ctg ttg ttg ctc ccg ccg ccg ctg ttg ctg ctg ctg ctg ccc tgt gag	240
Leu Leu Leu Leu Pro Pro Pro Leu Leu Leu Leu Leu Pro Cys Glu	
65 70 75 80	
gcc gag gcc gcg gcg gcg gcg gcg gcg gtg tgc ggc tca gcc gca gcc	288
Ala Glu Ala Ala Ala Ala Ala Ala Val Ser Gly Ser Ala Ala Ala	
85 90 95	
gag gcc aag gaa tgt gac ccg ccc tgt gtc aac ggc ggt cgc tgc aac	336
Glu Ala Lys Glu Cys Asp Arg Pro Cys Val Asn Gly Gly Arg Cys Asn	
100 105 110	
cct ggc acc ggc cag tgc gtc tgc ccc gcc ggc tgg gtg ggc gag caa	384
Pro Gly Thr Gly Gln Cys Val Cys Pro Ala Gly Trp Val Gly Glu Gln	
115 120 125	
tgc cag cac tgc ggg ggc cgc ttc aga cta act gga tct tct ggg ttt	432
Cys Gln His Cys Gly Gly Arg Phe Arg Leu Thr Gly Ser Ser Gly Phe	
130 135 140	
gtg aca gat gga cct gga aat tat aaa tac aaa acg aag tgc acg tgg	480
Val Thr Asp Gly Pro Gly Asn Tyr Lys Tyr Lys Thr Lys Cys Thr Trp	
145 150 155 160	
ctc att gaa gga cag cca aat aga ata atg aga ctt cgt ttc aat cat	528
Leu Ile Glu Gly Gln Pro Asn Arg Ile Met Arg Leu Arg Phe Asn His	
165 170 175	
ttt gct aca gag tgt agt tgg gac cat tta tat gtt tat gat ggg gac	576
Phe Ala Thr Glu Cys Ser Trp Asp His Leu Tyr Val Tyr Asp Gly Asp	
180 185 190	
tca att tat gca ccg cta gtt gct gca ttt agt ggc ctc att gtt cct	624
Ser Ile Tyr Ala Pro Leu Val Ala Ala Phe Ser Gly Leu Ile Val Pro	
195 200 205	
gag aga gat ggc aat gag act gtc cct gag gtt gtt gcc aca tca ggt	672
Glu Arg Asp Gly Asn Glu Thr Val Pro Glu Val Val Ala Thr Ser Gly	
210 215 220	
tat gcc ttg ctg cat ttt ttt agt gat gct gct tat aat ttg act gga	720
Tyr Ala Leu Leu His Phe Phe Ser Asp Ala Ala Tyr Asn Leu Thr Gly	
225 230 235 240	

ttt aat att act tac agt ttt gat atg tgt cca aat aac tgc tca ggc Phe Asn Ile Thr Tyr Ser Phe Asp Met Cys Pro Asn Asn Cys Ser Gly 245 250 255	768
cga gga gag tgt aag atc agt aat agc agc gaa act gtt gaa tgt gaa Arg Gly Glu Cys Lys Ile Ser Asn Ser Ser Glu Thr Val Glu Cys Glu 260 265 270	816
tgt tct gaa aac tgg aaa ggt gaa gca tgt gac att cct cac tgt aca Cys Ser Glu Asn Trp Lys Gly Glu Ala Cys Asp Ile Pro His Cys Thr 275 280 285	864
gac aac tgt ggt ttt cct cat cga ggc atc tgc aat tca agt gat gtc Asp Asn Cys Gly Phe Pro His Arg Gly Ile Cys Asn Ser Ser Asp Val 290 295 300	912
aga gga tgc tcc tgc ttc tca gac tgg cag ggt cct gga tgt tca gtt Arg Gly Cys Ser Cys Phe Ser Asp Trp Gln Gly Pro Gly Cys Ser Val 305 310 315 320	960
cct gta cca gct aac cag tca ttt tgg act cga gag gaa tat tct aac Pro Val Pro Ala Asn Gln Ser Phe Trp Thr Arg Glu Glu Tyr Ser Asn 325 330 335	1008
tta aag ctc ccc aga gca tct cat aaa gct gtg gtc aat gga aac att Leu Lys Leu Pro Arg Ala Ser His Lys Ala Val Val Asn Gly Asn Ile 340 345 350	1056
atg tgg gtt gtt gga gga tat atg ttc aac cac tca gat tat aac atg Met Trp Val Val Gly Gly Tyr Met Phe Asn His Ser Asp Tyr Asn Met 355 360 365	1104
gtt cta gcg tat gac ctt gct tct agg gag tgg ctt cca cta aac cgt Val Leu Ala Tyr Asp Leu Ala Ser Arg Glu Trp Leu Pro Leu Asn Arg 370 375 380	1152
tct gtg aac aat gtg gtt gtt aga tat ggt cat tct ttg gca tta tac Ser Val Asn Asn Val Val Arg Tyr Gly His Ser Leu Ala Leu Tyr 385 390 395 400	1200
aag gat aaa att tac atg tat gga gga aaa att gat cca act ggg aat Lys Asp Lys Ile Tyr Met Tyr Gly Gly Lys Ile Asp Pro Thr Gly Asn 405 410 415	1248
gtg acc aat gag ttg aga gtt ttt cac att cat aat gag tca tgg gtg Val Thr Asn Glu Leu Arg Val Phe His Ile His Asn Glu Ser Trp Val 420 425 430	1296
ttg ttg acc cct aag gca aag gag cag tat gca gtg gtt ggg cac tct Leu Leu Thr Pro Lys Ala Lys Glu Gln Tyr Ala Val Val Gly His Ser 435 440 445	1344
gca cac att gtt aca ctg aag aat ggc cga gtg gtc atg ctg gtc atc Ala His Ile Val Thr Leu Lys Asn Gly Arg Val Val Met Leu Val Ile 450 455 460	1392
ttt ggt cac tgc cct ctc tat gga tat ata agc aat gtg cag gaa tat Phe Gly His Cys Pro Leu Tyr Gly Tyr Ile Ser Asn Val Gln Glu Tyr 465 470 475 480	1440
gat ttg gat aag aac aca tgg agt ata tta cac acc cag ggt gcc ctt Asp Leu Asp Lys Asn Thr Trp Ser Ile Leu His Thr Gln Gly Ala Leu 485 490 495	1488

gtg caa ggg ggt tac ggc cat agc agt gtt tac gac cat agg acc agg Val Gln Gly Gly Tyr Gly His Ser Ser Val Tyr Asp His Arg Thr Arg 500 505 510	1536
gcc cta tac gtt cat ggt ggc tac aag gct ttc agt gcc aat aag tac Ala Leu Tyr Val His Gly Gly Tyr Lys Ala Phe Ser Ala Asn Lys Tyr 515 520 525	1584
cgg ctt gca gat gat ctc tac cga tat gat gtg gat acc cag atg tgg Arg Leu Ala Asp Asp Leu Tyr Arg Tyr Asp Val Asp Thr Gln Met Trp 530 535 540	1632
acc att ctt aag gac agc cga ttt ttc cgt tac ttg cac aca gct gtg Thr Ile Leu Lys Asp Ser Arg Phe Phe Arg Tyr Leu His Thr Ala Val 545 550 555 560	1680
ata gtg agt gga acc atg ctg gtg ttt ggg gga aac aca cac aat gac Ile Val Ser Gly Thr Met Leu Val Phe Gly Gly Asn Thr His Asn Asp 565 570 575	1728
aca tct atg agc cat ggc gcc aaa tgc ttc tct tca gat ttc atg gcc Thr Ser Met Ser His Gly Ala Lys Cys Phe Ser Ser Asp Phe Met Ala 580 585 590	1776
tat gac att gcc tgt gac cgc tgg tca gtg ctt ccc aga cct gat ctc Tyr Asp Ile Ala Cys Asp Arg Trp Ser Val Leu Pro Arg Pro Asp Leu 595 600 605	1824
cac cat gat gtc aac aga ttt ggc cat tca gca gtc tta cac aac agc His His Asp Val Asn Arg Phe Gly His Ser Ala Val Leu His Asn Ser 610 615 620	1872
acc atg tat gtg ttc ggt ggt ttc aat agt ctc ctc ctc agc gac atc Thr Met Tyr Val Phe Gly Gly Phe Asn Ser Leu Leu Leu Ser Asp Ile 625 630 635 640	1920
ctg gta ttc acc tcg gaa cag tgt gat gcg cat cgg agt gaa gcc gct Leu Val Phe Thr Ser Glu Gln Cys Asp Ala His Arg Ser Glu Ala Ala 645 650 655	1968
tgt tta gca gca gga cct ggt att cgg tgt gtg tgg aac aca ggg tcg Cys Leu Ala Ala Gly Pro Gly Ile Arg Cys Val Trp Asn Thr Gly Ser 660 665 670	2016
tct cag tgt atc tcg tgg gcg ctg gca act gat gaa caa gaa gaa aag Ser Gln Cys Ile Ser Trp Ala Leu Ala Thr Asp Glu Gln Glu Glu Lys 675 680 685	2064
tta aaa tca gaa tgt ttt tcc aaa aga act ctt gac cat gac aga tgt Leu Lys Ser Glu Cys Phe Ser Lys Arg Thr Leu Asp His Asp Arg Cys 690 695 700	2112
gac cag cac aca gat tgt tac agc tgt aca gcc aac acc aat gac tgc Asp Gln His Thr Asp Cys Tyr Ser Cys Thr Ala Asn Thr Asn Asp Cys 705 710 715 720	2160
cac tgg tgc aat gac cat tgt gtc ccc agg aac cac agc tgc tca gaa His Trp Cys Asn Asp His Cys Val Pro Arg Asn His Ser Cys Ser Glu 725 730 735	2208
ggc cag atc tcc att ttt agg tat gag aat tgc ccc aag gat aac ccc Gly Gln Ile Ser Ile Phe Arg Tyr Glu Asn Cys Pro Lys Asp Asn Pro 740 745 750	2256
atg tac tac tgt aac aag aag acc agc tgc agg agc tgt gcc ctg gac Met Tyr Tyr Cys Asn Lys Lys Thr Ser Cys Arg Ser Cys Ala Leu Asp 755 760 765	2304

cag aac tgc cag tgg gag ccc cgg aat cag gag tgc att gcc ctg ccc Gln Asn Cys Gln Trp Glu Pro Arg Asn Gln Glu Cys Ile Ala Leu Pro 770 775 780	2352
gaa aat atc tgt ggc att ggc tgg cat ttg gtt gga aac tca tgt ttg Glu Asn Ile Cys Gly Ile Gly Trp His Leu Val Gly Asn Ser Cys Leu 785 790 795 800	2400
aaa att act act gcc aag gag aat tat gac aat gct aaa ttg ttc tgt Lys Ile Thr Thr Ala Lys Glu Asn Tyr Asp Asn Ala Lys Leu Phe Cys 805 810 815	2448
agg aac cac aat gcc ctt ttg gct tct ctt aca acc cag aag aag gta Arg Asn His Asn Ala Leu Leu Ala Ser Leu Thr Thr Gln Lys Lys Val 820 825 830	2496
gaa ttt gtc ctt aag cag ctg cga ata atg cag tca tct cag agc atg Glu Phe Val Leu Lys Gln Leu Arg Ile Met Gln Ser Ser Gln Ser Met 835 840 845	2544
tcc aag ctc acc tta acc cca tgg gtc ggc ctt cgg aag atc aat gtg Ser Lys Leu Thr Leu Thr Pro Trp Val Gly Leu Arg Lys Ile Asn Val 850 855 860	2592
tcc tac tgg tgc tgg gaa gat atg tcc cca ttt aca aat agt tta cta Ser Tyr Trp Cys Trp Glu Asp Met Ser Pro Phe Thr Asn Ser Leu Leu 865 870 875 880	2640
cag tgg atg ccg tct gag ccc agt gat gct gga ttc tgt gga att tta Gln Trp Met Pro Ser Glu Pro Ser Asp Ala Gly Phe Cys Gly Ile Leu 885 890 895	2688
tca gaa ccc agt act cgg gga ctg aag gct gca acc tgc atc aac cca Ser Glu Pro Ser Thr Arg Gly Leu Lys Ala Ala Thr Cys Ile Asn Pro 900 905 910	2736
ctc aat ggt agt gtc tgt gaa agg cct gca aac cac agt gct aag cag Leu Asn Gly Ser Val Cys Glu Arg Pro Ala Asn His Ser Ala Lys Gln 915 920 925	2784
tgc cgg aca cca tgt gcc ttg agg aca gca tgt gga gat tgc acc agc Cys Arg Thr Pro Cys Ala Leu Arg Thr Ala Cys Gly Asp Cys Thr Ser 930 935 940	2832
ggc agc tct gag tgc atg tgg tgc agc aac atg aag cag tgt gtg gac Gly Ser Ser Glu Cys Met Trp Cys Ser Asn Met Lys Gln Cys Val Asp 945 950 955 960	2880
tcc aat gcc tat gtg gcc tcc ttc cct ttt ggc cag tgt atg gaa tgg Ser Asn Ala Tyr Val Ala Ser Phe Pro Phe Gly Gln Cys Met Glu Trp 965 970 975	2928
tat acg atg agc acc tgc ccc cct gaa aat tgt tca ggc tac tgt acc Tyr Thr Met Ser Thr Cys Pro Pro Glu Asn Cys Ser Gly Tyr Cys Thr 980 985 990	2976
tgt agt cat tgc ttg gag caa cca ggc tgt ggc tgg tgt act gat ccc Cys Ser His Cys Leu Glu Gln Pro Gly Cys Gly Trp Cys Thr Asp Pro 995 1000 1005	3024
agc aat act ggc aaa ggg aaa tgc ata gag ggt tcc tat aaa gga cca Ser Asn Thr Gly Lys Gly Lys Cys Ile Glu Gly Ser Tyr Lys Gly Pro 1010 1015 1020	3072

gtg aag atg cct tcg caa gcc cct aca gga aat ttc tat cca cag ccc Val Lys Met Pro Ser Gln Ala Pro Thr Gly Asn Phe Tyr Pro Gln Pro 1025 1030 1035 1040	3120
ctg ctc aat tcc agc atg tgt cta gag gac agc aga tac aac tgg tct Leu Leu Asn Ser Ser Met Cys Leu Glu Asp Ser Arg Tyr Asn Trp Ser 1045 1050 1055	3168
ttc att cac tgt cca gct tgc caa tgc aac ggc cac agt aaa tgc atc Phe Ile His Cys Pro Ala Cys Gln Cys Asn Gly His Ser Lys Cys Ile 1060 1065 1070	3216
aat cag agc atc tgt gag aag tgt gag aac ctg acc aca ggc aag cac Asn Gln Ser Ile Cys Glu Lys Cys Glu Asn Leu Thr Thr Gly Lys His 1075 1080 1085	3264
tgc gag acc tgc ata tct ggc ttc tac ggt gat ccc acc aat gga ggg Cys Glu Thr Cys Ile Ser Gly Phe Tyr Gly Asp Pro Thr Asn Gly Gly 1090 1095 1100	3312
aaa tgt cag cca tgc aag tgc aat ggg cac gcg tct ctg tgc aac acc Lys Cys Gln Pro Cys Lys Cys Asn Gly His Ala Ser Leu Cys Asn Thr 1105 1110 1115 1120	3360
aac acg ggc aag tgc ttc tgc acc acc aag ggc gtc aag ggg gac gag Asn Thr Gly Lys Cys Phe Cys Thr Thr Lys Gly Val Lys Gly Asp Glu 1125 1130 1135	3408
tgc cag cta tgt gag gta gaa aat cga tac caa gga aac cct ctc aga Cys Gln Leu Cys Glu Val Glu Asn Arg Tyr Gln Gly Asn Pro Leu Arg 1140 1145 1150	3456
gga aca tgt tat tat act ctt ctt att gac tat cag ttc acc ttt agt Gly Thr Cys Tyr Tyr Thr Leu Leu Ile Asp Tyr Gln Phe Thr Phe Ser 1155 1160 1165	3504
cta tcc cag gaa gat gat cgc tat tac aca gct atc aat ttt gtg gct Leu Ser Gln Glu Asp Asp Arg Tyr Thr Ala Ile Asn Phe Val Ala 1170 1175 1180	3552
act cct gac gaa caa aac agg gat ttg gac atg ttc atc aat gcc tcc Thr Pro Asp Glu Gln Asn Arg Asp Leu Asp Met Phe Ile Asn Ala Ser 1185 1190 1195 1200	3600
aag aat ttc aac ctc aac atc acc tgg gct gcc agt ttc tca gct gga Lys Asn Phe Asn Leu Asn Ile Thr Trp Ala Ala Ser Phe Ser Ala Gly 1205 1210 1215	3648
acc cag gct gga gaa gag atg cct gtt gtt tca aaa acc aac att aag Thr Gln Ala Gly Glu Glu Met Pro Val Val Ser Lys Thr Asn Ile Lys 1220 1225 1230	3696
gag tac aaa gat agt ttc tct aat gag aag ttt gat ttt cgc aac cac Glu Tyr Lys Asp Ser Phe Ser Asn Glu Lys Phe Asp Phe Arg Asn His 1235 1240 1245	3744
cca aat atc act ttc ttt gtt tat gtc agt aat ttc acc tgg ccc atc Pro Asn Ile Thr Phe Phe Val Tyr Val Ser Asn Phe Thr Trp Pro Ile 1250 1255 1260	3792
aaa att cag att gcc ttc tct cag cac agc aat ttt atg gac ctg gta Lys Ile Gln Ile Ala Phe Ser Gln His Ser Asn Phe Met Asp Leu Val 1265 1270 1275 1280	3840
cag ttc ttc gtg act ttc ttc agt tgt ttc ctc tct ttg ctc ctg gtg Gln Phe Phe Val Thr Phe Phe Ser Cys Phe Leu Ser Leu Leu Val 1285 1290 1295	3888



25

gct gct gtg gtt tgg aag atc aaa caa agt tgt tgg gcc tcc aga cgt 3936  
 Ala Ala Val Val Trp Lys Ile Lys Gln Ser Cys Trp Ala Ser Arg Arg  
 1300 1305 1310

aga gag caa ctt ctt cga gag atg caa cag atg gcc agc cgt ccc ttt 3984  
 Arg Glu Gln Leu Leu Arg Glu Met Gln Gln Met Ala Ser Arg Pro Phe  
 1315 1320 1325

gcc tct gta aat gtc gcc ttg gaa aca gat gag gag cct cct gat ctt 4032  
 Ala Ser Val Asn Val Ala Leu Glu Thr Asp Glu Glu Pro Pro Asp Leu  
 1330 1335 1340

att ggg ggg agt ata aag act gtt ccc aaa ccc att gca ctg gag ccg 4080  
 Ile Gly Gly Ser Ile Lys Thr Val Pro Lys Pro Ile Ala Leu Glu Pro  
 1345 1350 1355 1360

tgt ttt ggc aac aaa gcc gct gtc ctc tct gtg ttt gtg agg ctc cct 4128  
 Cys Phe Gly Asn Lys Ala Ala Val Leu Ser Val Phe Val Arg Leu Pro  
 1365 1370 1375

cga ggc ctg ggt ggc atc cct cct cct ggg cag tca ggt ctt gct gtg 4176  
 Arg Gly Leu Gly Gly Ile Pro Pro Pro Gly Gln Ser Gly Leu Ala Val  
 1380 1385 1390

gcc agc gcc ctg gtg gac att tct cag cag atg ccg ata gtg tac aag 4224  
 Ala Ser Ala Leu Val Asp Ile Ser Gln Gln Met Pro Ile Val Tyr Lys  
 1395 1400 1405

gag aag tca gga gcc gtg aga aac cgg aag cag cag ccc cct gca cag 4272  
 Glu Lys Ser Gly Ala Val Arg Asn Arg Lys Gln Gln Pro Pro Ala Gln  
 1410 1415 1420

cct ggg acc tgc atc tga 4290  
 Pro Gly Thr Cys Ile  
 1425

<210> 14  
 <211> 25  
 <212> PRT  
 <213> Homo sapiens

<400> 14  
 Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val  
 1 5 10 15  
 Leu Met Ser Ala Gln Glu Ser Trp Ala  
 20 25

<210> 15  
 <211> 5  
 <212> PRT  
 <213> Bovidae

<400> 15  
 Lys Phe Glu Arg Gln  
 1 5

<210> 16  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
 Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro  
 1 5 10 15

<210> 17  
 <211> 4  
 <212> PRT  
 <213> Rattus rattus

<400> 17  
 Lys Asp Glu Leu  
 1

<210> 18  
 <211> 1272  
 <212> PRT  
 <213> Homo sapiens

<400> 18  
 Met Val Ala Ala Ala Ala Thr Glu Ala Arg Leu Arg Arg Arg Thr  
 1 5 10 15  
 Ala Ala Thr Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Trp Asp  
 20 25 30  
 Trp Asp Val Thr Arg Ala Gly Arg Pro Gly Leu Gly Ala Gly Leu Arg  
 35 40 45  
 Leu Pro Arg Leu Leu Ser Pro Pro Leu Arg Pro Arg Leu Leu Leu Leu  
 50 55 60  
 Leu Leu Leu Leu Pro Pro Pro Leu Leu Leu Leu Leu Pro Cys Glu  
 65 70 75 80  
 Ala Glu Ala Ala Ala Ala Ala Ala Val Ser Gly Ser Ala Ala Ala  
 85 90 95  
 Glu Ala Lys Glu Cys Asp Arg Pro Cys Val Asn Gly Gly Arg Cys Asn  
 100 105 110  
 Pro Gly Thr Gly Gln Cys Val Cys Pro Ala Gly Trp Val Gly Glu Gln  
 115 120 125  
 Cys Gln His Cys Gly Gly Arg Phe Arg Leu Thr Gly Ser Ser Gly Phe  
 130 135 140  
 Val Thr Asp Gly Pro Gly Asn Tyr Lys Tyr Lys Thr Lys Cys Thr Trp  
 145 150 155 160  
 Leu Ile Glu Gly Gln Pro Asn Arg Ile Met Arg Leu Arg Phe Asn His  
 165 170 175  
 Phe Ala Thr Glu Cys Ser Trp Asp His Leu Tyr Val Tyr Asp Gly Asp  
 180 185 190  
 Ser Ile Tyr Ala Pro Leu Val Ala Ala Phe Ser Gly Leu Ile Val Pro  
 195 200 205  
 Glu Arg Asp Gly Asn Glu Thr Val Pro Glu Val Val Ala Thr Ser Gly  
 210 215 220  
 Tyr Ala Leu Leu His Phe Phe Ser Asp Ala Ala Tyr Asn Leu Thr Gly  
 225 230 235 240  
 Phe Asn Ile Thr Tyr Ser Phe Asp Met Cys Pro Asn Asn Cys Ser Gly  
 245 250 255  
 Arg Gly Glu Cys Lys Ile Ser Asn Ser Ser Glu Thr Val Glu Cys Glu  
 260 265 270  
 Cys Ser Glu Asn Trp Lys Gly Glu Ala Cys Asp Ile Pro His Cys Thr  
 275 280 285  
 Asp Asn Cys Gly Phe Pro His Arg Gly Ile Cys Asn Ser Ser Asp Val  
 290 295 300  
 Arg Gly Cys Ser Cys Phe Ser Asp Trp Gln Gly Pro Gly Cys Ser Val  
 305 310 315 320  
 Pro Val Pro Ala Asn Gln Ser Phe Trp Thr Arg Glu Glu Tyr Ser Asn  
 325 330 335  
 Leu Lys Leu Pro Arg Ala Ser His Lys Ala Val Val Asn Gly Asn Ile  
 340 345 350  
 Met Trp Val Val Gly Gly Tyr Met Phe Asn His Ser Asp Tyr Asn Met  
 355 360 365  
 Val Leu Ala Tyr Asp Leu Ala Ser Arg Glu Trp Leu Pro Leu Asn Arg  
 370 375 380  
 Ser Val Asn Asn Val Val Val Arg Tyr Gly His Ser Leu Ala Leu Tyr  
 385 390 395 400  
 Lys Asp Lys Ile Tyr Met Tyr Gly Gly Lys Ile Asp Pro Thr Gly Asn  
 405 410 415

Val Thr Asn Glu Leu Arg Val Phe His Ile His Asn Glu Ser Trp Val  
 420 425 430  
 Leu Leu Thr Pro Lys Ala Lys Glu Gln Tyr Ala Val Val Gly His Ser  
 435 440 445  
 Ala His Ile Val Thr Leu Lys Asn Gly Arg Val Val Met Leu Val Ile  
 450 455 460  
 Phe Gly His Cys Pro Leu Tyr Gly Tyr Ile Ser Asn Val Gln Glu Tyr  
 465 470 475 480  
 Asp Leu Asp Lys Asn Thr Trp Ser Ile Leu His Thr Gln Gly Ala Leu  
 485 490 495  
 Val Gln Gly Gly Tyr Gly His Ser Ser Val Tyr Asp His Arg Thr Arg  
 500 505 510  
 Ala Leu Tyr Val His Gly Gly Tyr Lys Ala Phe Ser Ala Asn Lys Tyr  
 515 520 525  
 Arg Leu Ala Asp Asp Leu Tyr Arg Tyr Asp Val Asp Thr Gln Met Trp  
 530 535 540  
 Thr Ile Leu Lys Asp Ser Arg Phe Phe Arg Tyr Leu His Thr Ala Val  
 545 550 555 560  
 Ile Val Ser Gly Thr Met Leu Val Phe Gly Gly Asn Thr His Asn Asp  
 565 570 575  
 Thr Ser Met Ser His Gly Ala Lys Cys Phe Ser Ser Asp Phe Met Ala  
 580 585 590  
 Tyr Asp Ile Ala Cys Asp Arg Trp Ser Val Leu Pro Arg Pro Asp Leu  
 595 600 605  
 His His Asp Val Asn Arg Phe Gly His Ser Ala Val Leu His Asn Ser  
 610 615 620  
 Thr Met Tyr Val Phe Gly Phe Asn Ser Leu Leu Ser Asp Ile  
 625 630 635 640  
 Leu Val Phe Thr Ser Glu Gln Cys Asp Ala His Arg Ser Glu Ala Ala  
 645 650 655  
 Cys Leu Ala Ala Gly Pro Gly Ile Arg Cys Val Trp Asn Thr Gly Ser  
 660 665 670  
 Ser Gln Cys Ile Ser Trp Ala Leu Ala Thr Asp Glu Gln Glu Lys  
 675 680 685  
 Leu Lys Ser Glu Cys Phe Ser Lys Arg Thr Leu Asp His Asp Arg Cys  
 690 695 700  
 Asp Gln His Thr Asp Cys Tyr Ser Cys Thr Ala Asn Thr Asn Asp Cys  
 705 710 715 720  
 His Trp Cys Asn Asp His Cys Val Pro Arg Asn His Ser Cys Ser Glu  
 725 730 735  
 Gly Gln Ile Ser Ile Phe Arg Tyr Glu Asn Cys Pro Lys Asp Asn Pro  
 740 745 750  
 Met Tyr Tyr Cys Asn Lys Lys Thr Ser Cys Arg Ser Cys Ala Leu Asp  
 755 760 765  
 Gln Asn Cys Gln Trp Glu Pro Arg Asn Gln Glu Cys Ile Ala Leu Pro  
 770 775 780  
 Glu Asn Ile Cys Gly Ile Gly Trp His Leu Val Gly Asn Ser Cys Leu  
 785 790 795 800  
 Lys Ile Thr Thr Ala Lys Glu Asn Tyr Asp Asn Ala Lys Leu Phe Cys  
 805 810 815  
 Arg Asn His Asn Ala Leu Leu Ala Ser Leu Thr Thr Gln Lys Lys Val  
 820 825 830  
 Glu Phe Val Leu Lys Gln Leu Arg Ile Met Gln Ser Ser Gln Ser Met  
 835 840 845  
 Ser Lys Leu Thr Leu Thr Pro Trp Val Gly Leu Arg Lys Ile Asn Val  
 850 855 860  
 Ser Tyr Trp Cys Trp Glu Asp Met Ser Pro Phe Thr Asn Ser Leu Leu  
 865 870 875 880  
 Gln Trp Met Pro Ser Glu Pro Ser Asp Ala Gly Phe Cys Gly Ile Leu  
 885 890 895  
 Ser Glu Pro Ser Thr Arg Gly Leu Lys Ala Ala Thr Cys Ile Asn Pro  
 900 905 910  
 Leu Asn Gly Ser Val Cys Glu Arg Pro Ala Asn His Ser Ala Lys Gln  
 915 920 925  
 Cys Arg Thr Pro Cys Ala Leu Arg Thr Ala Cys Gly Asp Cys Thr Ser  
 930 935 940

Gly Ser Ser Glu Cys Met Trp Cys Ser Asn Met Lys Gln Cys Val Asp  
 945 950 955 960  
 Ser Asn Ala Tyr Val Ala Ser Phe Pro Phe Gly Gln Cys Met Glu Trp  
 965 970 975  
 Tyr Thr Met Ser Thr Cys Pro Pro Glu Asn Cys Ser Gly Tyr Cys Thr  
 980 985 990  
 Cys Ser His Cys Leu Glu Gln Pro Gly Cys Gly Trp Cys Thr Asp Pro  
 995 1000 1005  
 Ser Asn Thr Gly Lys Gly Lys Cys Ile Glu Gly Ser Tyr Lys Gly Pro  
 1010 1015 1020  
 Val Lys Met Pro Ser Gln Ala Pro Thr Gly Asn Phe Tyr Pro Gln Pro  
 1025 1030 1035 1040  
 Leu Leu Asn Ser Ser Met Cys Leu Glu Asp Ser Arg Tyr Asn Trp Ser  
 1045 1050 1055  
 Phe Ile His Cys Pro Ala Cys Gln Cys Asn Gly His Ser Lys Cys Ile  
 1060 1065 1070  
 Asn Gln Ser Ile Cys Glu Lys Cys Glu Asn Leu Thr Thr Gly Lys His  
 1075 1080 1085  
 Cys Glu Thr Cys Ile Ser Gly Phe Tyr Gly Asp Pro Thr Asn Gly Gly  
 1090 1095 1100  
 Lys Cys Gln Pro Cys Lys Cys Asn Gly His Ala Ser Leu Cys Asn Thr  
 1105 1110 1115 1120  
 Asn Thr Gly Lys Cys Phe Cys Thr Thr Lys Gly Val Lys Gly Asp Glu  
 1125 1130 1135  
 Cys Gln Leu Cys Glu Val Glu Asn Arg Tyr Gln Gly Asn Pro Leu Arg  
 1140 1145 1150  
 Gly Thr Cys Tyr Tyr Thr Leu Leu Ile Asp Tyr Gln Phe Thr Phe Ser  
 1155 1160 1165  
 Leu Ser Gln Glu Asp Asp Arg Tyr Tyr Thr Ala Ile Asn Phe Val Ala  
 1170 1175 1180  
 Thr Pro Asp Glu Gln Asn Arg Asp Leu Asp Met Phe Ile Asn Ala Ser  
 1185 1190 1195 1200  
 Lys Asn Phe Asn Leu Asn Ile Thr Trp Ala Ala Ser Phe Ser Ala Gly  
 1205 1210 1215  
 Thr Gln Ala Gly Glu Glu Met Pro Val Val Ser Lys Thr Asn Ile Lys  
 1220 1225 1230  
 Glu Tyr Lys Asp Ser Phe Ser Asn Glu Lys Phe Asp Phe Arg Asn His  
 1235 1240 1245  
 Pro Asn Ile Thr Phe Phe Val Tyr Val Ser Asn Phe Thr Trp Pro Ile  
 1250 1255 1260  
 Lys Ile Gln Val Gln Thr Glu Gln  
 1265 1270

<210> 19  
 <211> 3819  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(3816)

<400> 19  
 atg gtg gcc gca gcg gcg gca act gag gca agg ctg agg agg agg acg 48  
 Met Val Ala Ala Ala Ala Thr Glu Ala Arg Leu Arg Arg Arg Thr  
 1 5 10 15  
 gcg gcg acg gca gcg ctc gcg ggc agg agc ggc ggg ccg cac tgg gac 96  
 Ala Ala Thr Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Trp Asp  
 20 25 30  
 tgg gac gtg acc agg gct ggg agg ccg ggg ctg ggg gcc ggg ctg cgc 144  
 Trp Asp Val Thr Arg Ala Gly Arg Pro Gly Leu Gly Ala Gly Leu Arg  
 35 40 45

ctc ccg cgg ctg ctg tct cca ccg ctg cgg cca cgg ctg ctg ctg ctg Leu Pro Arg Leu Leu Ser Pro Pro Leu Arg Pro Arg Leu Leu Leu Leu 50 55 60	192
ctg ttg ttg ctc ccg ccg ccg ctg ttg ctg ctg ctg ccc tgt gag Leu Leu Leu Leu Pro Pro Pro Leu Leu Leu Leu Leu Leu Pro Cys Glu 65 70 75 80	240
gcc gag gcc gcg gcg gcg gcg gcg gcg gtg tgc ggc tca gcc gca gcc Ala Glu Ala Ala Ala Ala Ala Ala Ala Val Ser Gly Ser Ala Ala Ala 85 90 95	288
gag gcc aag gaa tgt gac cgg ccc tgt gtc aac ggc ggt cgc tgc aac Glu Ala Lys Glu Cys Asp Arg Pro Cys Val Asn Gly Gly Arg Cys Asn 100 105 110	336
cct ggc acc ggc cag tgc gtc tgc ccc gcc ggc tgg gtg ggc gag caa Pro Gly Thr Gly Gln Cys Val Cys Pro Ala Gly Trp Val Gly Glu Gln 115 120 125	384
tgc cag cac tgc ggg ggc cgc ttc aga cta act gga tct tct ggg ttt Cys Gln His Cys Gly Gly Arg Phe Arg Leu Thr Gly Ser Ser Gly Phe 130 135 140	432
gtg aca gat gga cct gga aat tat aaa tac aaa acg aag tgc acg tgg Val Thr Asp Gly Pro Gly Asn Tyr Lys Tyr Lys Thr Lys Cys Thr Trp 145 150 155 160	480
ctc att gaa gga cag cca aat aga ata atg aga ctt cgt ttc aat cat Leu Ile Glu Gly Gln Pro Asn Arg Ile Met Arg Leu Arg Phe Asn His 165 170 175	528
ttt gct aca gag tgt agt tgg gac cat tta tat gtt tat gat ggg gac Phe Ala Thr Glu Cys Ser Trp Asp His Leu Tyr Val Tyr Asp Gly Asp 180 185 190	576
tca att tat gca ccg cta gtt gct gca ttt agt ggc ctc att gtt cct Ser Ile Tyr Ala Pro Leu Val Ala Ala Phe Ser Gly Leu Ile Val Pro 195 200 205	624
gag aga gat ggc aat gag act gtc cct gag gtt gtt gcc aca tca ggt Glu Arg Asp Gly Asn Glu Thr Val Pro Glu Val Val Ala Thr Ser Gly 210 215 220	672
tat gcc ttg ctg cat ttt ttt agt gat gct gct tat aat ttg act gga Tyr Ala Leu Leu His Phe Phe Ser Asp Ala Tyr Asn Leu Thr Gly 225 230 235 240	720
ttt aat att act tac agt ttt gat atg tgt cca aat aac tgc tca ggc Phe Asn Ile Thr Tyr Ser Phe Asp Met Cys Pro Asn Asn Cys Ser Gly 245 250 255	768
cga gga gag tgt aag atc agt aat agc agc gaa act gtt gaa tgt gaa Arg Gly Glu Cys Lys Ile Ser Asn Ser Ser Glu Thr Val Glu Cys Glu 260 265 270	816
tgt tct gaa aac tgg aaa ggt gaa gca tgt gac att cct cac tgt aca Cys Ser Glu Asn Trp Lys Gly Glu Ala Cys Asp Ile Pro His Cys Thr 275 280 285	864
gac aac tgt ggt ttt cct cat cga ggc atc tgc aat tca agt gat gtc Asp Asn Cys Gly Phe Pro His Arg Gly Ile Cys Asn Ser Ser Asp Val 290 295 300	912
aga gga tgc tcc tgc ttc tca gac tgg cag ggt cct gga tgt tca gtt Arg Gly Cys Ser Cys Phe Ser Asp Trp Gln Gly Pro Gly Cys Ser Val 305 310 315 320	960

cct gta cca gct aac cag tca ttt tgg act cga gag gaa tat tct aac Pro Val Pro Ala Asn Gln Ser Phe Trp Thr Arg Glu Glu Tyr Ser Asn 325 330 335	1008
tta aag ctc ccc aga gca tct cat aaa gct gtg gtc aat gga aac att Leu Lys Leu Pro Arg Ala Ser His Lys Ala Val Val Asn Gly Asn Ile 340 345 350	1056
atg tgg gtt gtt gga gga tat atg ttc aac cac tca gat tat aac atg Met Trp Val Val Gly Gly Tyr Met Phe Asn His Ser Asp Tyr Asn Met 355 360 365	1104
gtt cta gcg tat gac ctt gct tct agg gag tgg ctt cca cta aac cgt Val Leu Ala Tyr Asp Leu Ala Ser Arg Glu Trp Leu Pro Leu Asn Arg 370 375 380	1152
tct gtg aac aat gtg gtt gtt aga tat ggt cat tct ttg gca tta tac Ser Val Asn Asn Val Val Arg Tyr Gly His Ser Leu Ala Leu Tyr 385 390 395 400	1200
aag gat aaa att tac atg tat gga gga aaa att gat cca act ggg aat Lys Asp Lys Ile Tyr Met Tyr Gly Gly Lys Ile Asp Pro Thr Gly Asn 405 410 415	1248
gtg acc aat gag ttg aga gtt ttt cac att cat aat gag tca tgg gtg Val Thr Asn Glu Leu Arg Val Phe His Ile His Asn Glu Ser Trp Val 420 425 430	1296
ttg ttg acc cct aag gca aag gag cag tat gca gtg gtt ggg cac tct Leu Leu Thr Pro Lys Ala Lys Glu Gln Tyr Ala Val Val Gly His Ser 435 440 445	1344
gca cac att gtt aca ctg aag aat ggc cga gtg gtc atg ctg gtc atc Ala His Ile Val Thr Leu Lys Asn Gly Arg Val Val Met Leu Val Ile 450 455 460	1392
ttt ggt cac tgc cct ctc tat gga tat ata agc aat gtg cag gaa tat Phe Gly His Cys Pro Leu Tyr Gly Tyr Ile Ser Asn Val Gln Glu Tyr 465 470 475 480	1440
gat ttg gat aag aac aca tgg agt ata tta cac acc cag ggt gcc ctt Asp Leu Asp Lys Asn Thr Trp Ser Ile Leu His Thr Gln Gly Ala Leu 485 490 495	1488
gtg caa ggg ggt tac ggc cat agc agt gtt tac gac cat agg acc agg Val Gln Gly Gly Tyr Gly His Ser Ser Val Tyr Asp His Arg Thr Arg 500 505 510	1536
gcc cta tac gtt cat ggt ggc tac aag gct ttc agt gcc aat aag tac Ala Leu Tyr Val His Gly Gly Tyr Lys Ala Phe Ser Ala Asn Lys Tyr 515 520 525	1584
cgg ctt gca gat gat ctc tac cga tat gat gtg gat acc cag atg tgg Arg Leu Ala Asp Asp Leu Tyr Arg Tyr Asp Val Asp Thr Gln Met Trp 530 535 540	1632
acc att ctt aag gac agc cga ttt ttc cgt tac ttg cac aca gct gtg Thr Ile Leu Lys Asp Ser Arg Phe Phe Arg Tyr Leu His Thr Ala Val 545 550 555 560	1680
ata gtg agt gga acc atg ctg gtg ttt ggg gga aac aca cac aat gac Ile Val Ser Gly Thr Met Leu Val Phe Gly Gly Asn Thr His Asn Asp 565 570 575	1728

aca tct atg agc cat ggc gcc aaa tgc ttc tct tca gat ttc atg gcc Thr Ser Met Ser His Gly Ala Lys Cys Phe Ser Ser Asp Phe Met Ala 580 585 590	1776
tat gac att gcc tgt gac cgc tgg tca gtg ctt ccc aga cct gat ctc Tyr Asp Ile Ala Cys Asp Arg Trp Ser Val Leu Pro Arg Pro Asp Leu 595 600 605	1824
cac cat gat gtc aac aga ttt ggc cat tca gca gtc tta cac aac agc His Asp Val Asn Arg Phe Gly His Ser Ala Val Leu His Asn Ser 610 615 620	1872
acc atg tat gtg ttc ggt ggt ttc aat agt ctc ctc ctc agc gac atc Thr Met Tyr Val Phe Gly Gly Phe Asn Ser Leu Leu Leu Ser Asp Ile 625 630 635 640	1920
ctg gta ttc acc tcg gaa cag tgt gat gcg cat cgg agt gaa gcc gct Leu Val Phe Thr Ser Glu Gln Cys Asp Ala His Arg Ser Glu Ala Ala 645 650 655	1968
tgt tta gca gca gga cct ggt att cgg tgt gtg tgg aac aca ggg tcg Cys Leu Ala Ala Gly Pro Gly Ile Arg Cys Val Trp Asn Thr Gly Ser 660 665 670	2016
tct cag tgt atc tcg tgg gcg ctg gca act gat gaa caa gaa gaa aag Ser Gln Cys Ile Ser Trp Ala Leu Ala Thr Asp Glu Gln Glu Lys 675 680 685	2064
tta aaa tca gaa tgt ttt tcc aaa aga act ctt gac cat gac aga tgt Leu Lys Ser Glu Cys Phe Ser Lys Arg Thr Leu Asp His Asp Arg Cys 690 695 700	2112
gac cag cac aca gat tgt tac agc tgt aca gcc aac acc aat gac tgc Asp Gln His Thr Asp Cys Tyr Ser Cys Thr Ala Asn Thr Asn Asp Cys 705 710 715 720	2160
cac tgg tgc aat gac cat tgt gtc ccc agg aac cac agc tgc tca gaa His Trp Cys Asn Asp His Cys Val Pro Arg Asn His Ser Cys Ser Glu 725 730 735	2208
ggc cag atc tcc att ttt agg tat gag aat tgc ccc aag gat aac ccc Gly Gln Ile Ser Ile Phe Arg Tyr Glu Asn Cys Pro Lys Asp Asn Pro 740 745 750	2256
atg tac tac tgt aac aag aag acc agc tgc agg agc tgt gcc ctg gac Met Tyr Tyr Cys Asn Lys Lys Thr Ser Cys Arg Ser Cys Ala Leu Asp 755 760 765	2304
cag aac tgc cag tgg gag ccc cgg aat cag gag tgc att gcc ctg ccc Gln Asn Cys Gln Trp Glu Pro Arg Asn Gln Glu Cys Ile Ala Leu Pro 770 775 780	2352
gaa aat atc tgt ggc att ggc tgg cat ttg gtt gga aac tca tgt ttg Glu Asn Ile Cys Gly Ile Gly Trp His Leu Val Gly Asn Ser Cys Leu 785 790 795 800	2400
aaa att act act gcc aag gag aat tat gac aat gct aaa ttg ttc tgt Lys Ile Thr Thr Ala Lys Glu Asn Tyr Asp Asn Ala Lys Leu Phe Cys 805 810 815	2448
agg aac cac aat gcc ctt ttg gct tct ctt aca acc cag aag aag gta Arg Asn His Asn Ala Leu Leu Ala Ser Leu Thr Thr Gln Lys Lys Val 820 825 830	2496
gaa ttt gtc ctt aag cag ctg cga ata atg cag tca tct cag agc atg Glu Phe Val Leu Lys Gln Leu Arg Ile Met Gln Ser Ser Gln Ser Met 835 840 845	2544

tcc aag ctc acc tta acc cca tgg gtc ggc ctt cgg aag atc aat gtg Ser Lys Leu Thr Leu Thr Pro Trp Val Gly Leu Arg Lys Ile Asn Val 850 855 860	2592
tcc tac tgg tgc tgg gaa gat atg tcc cca ttt aca aat agt tta cta Ser Tyr Trp Cys Trp Glu Asp Met Ser Pro Phe Thr Asn Ser Leu Leu 865 870 875 880	2640
cag tgg atg ccg tct gag ccc agt gat gct gga ttc tgt gga att tta Gln Trp Met Pro Ser Glu Pro Ser Asp Ala Gly Phe Cys Gly Ile Leu 885 890 895	2688
tca gaa ccc agt act cgg gga ctg aag gct gca acc tgc atc aac cca Ser Glu Pro Ser Thr Arg Gly Leu Lys Ala Ala Thr Cys Ile Asn Pro 900 905 910	2736
ctc aat ggt agt gtc tgt gaa agg cct gca aac cac agt gct aag cag Leu Asn Gly Ser Val Cys Glu Arg Pro Ala Asn His Ser Ala Lys Gln 915 920 925	2784
tgc cgg aca cca tgt gcc ttg agg aca gca tgt gga gat tgc acc agc Cys Arg Thr Pro Cys Ala Leu Arg Thr Ala Cys Gly Asp Cys Thr Ser 930 935 940	2832
ggc agc tct gag tgc atg tgg tgc agc aac atg aag cag tgt gtg gac Gly Ser Ser Glu Cys Met Trp Cys Ser Asn Met Lys Gln Cys Val Asp 945 950 955 960	2880
tcc aat gcc tat gtg gcc tcc ttc cct ttt ggc cag tgt atg gaa tgg Ser Asn Ala Tyr Val Ala Ser Phe Pro Phe Gly Gln Cys Met Glu Trp 965 970 975	2928
tat acg atg agc acc tgc ccc cct gaa aat tgt tca ggc tac tgt acc Tyr Thr Met Ser Thr Cys Pro Pro Glu Asn Cys Ser Gly Tyr Cys Thr 980 985 990	2976
tgt agt cat tgc ttg gag caa cca ggc tgt ggc tgg tgt act gat ccc Cys Ser His Cys Leu Glu Gln Pro Gly Cys Gly Trp Cys Thr Asp Pro 995 1000 1005	3024
agc aat act ggc aaa ggg aaa tgc ata gag ggt tcc tat aaa gga cca Ser Asn Thr Gly Lys Gly Lys Cys Ile Glu Gly Ser Tyr Lys Gly Pro 1010 1015 1020	3072
gtg aag atg cct tcg caa gcc cct aca gga aat ttc tat cca cag ccc Val Lys Met Pro Ser Gln Ala Pro Thr Gly Asn Phe Tyr Pro Gln Pro 1025 1030 1035 1040	3120
ctg ctc aat tcc agc atg tgt cta gag gac agc aga tac aac tgg tct Leu Leu Asn Ser Ser Met Cys Leu Glu Asp Ser Arg Tyr Asn Trp Ser 1045 1050 1055	3168
ttc att cac tgt cca gct tgc caa tgc aac ggc cac agt aaa tgc atc Phe Ile His Cys Pro Ala Cys Gln Cys Asn Gly His Ser Lys Cys Ile 1060 1065 1070	3216
aat cag agc atc tgt gag aag tgt gag aac ctg acc aca ggc aag cac Asn Gln Ser Ile Cys Glu Lys Cys Glu Asn Leu Thr Thr Gly Lys His 1075 1080 1085	3264
tgc gag acc tgc ata tct ggc ttc tac ggt gat ccc acc aat gga ggg Cys Glu Thr Cys Ile Ser Gly Phe Tyr Gly Asp Pro Thr Asn Gly Gly 1090 1095 1100	3312



aaa tgt cag cca tgc aag tgc aat ggg cac gcg tct ctg tgc aac acc 3360  
 Lys Cys Gln Pro Cys Lys Cys Asn Gly His Ala Ser Leu Cys Asn Thr 1120  
 1105 1110 1115  
 aac acg ggc aag tgc ttc tgc acc acc aag ggc gtc aag ggg gac gag 3408  
 Asn Thr Gly Lys Cys Phe Cys Thr Thr Lys Gly Val Lys Gly Asp Glu 1135  
 1125 1130  
 tgc cag cta tgt gag gta gaa aat cga tac caa gga aac cct ctc aga 3456  
 Cys Gln Leu Cys Glu Val Glu Asn Arg Tyr Gln Gly Asn Pro Leu Arg 1150  
 1140 1145  
 gga aca tgt tat tat act ctt ctt att gac tat cag ttc acc ttt agt 3504  
 Gly Thr Cys Tyr Tyr Thr Leu Leu Ile Asp Tyr Gln Phe Thr Phe Ser 1165  
 1155 1160  
 cta tcc cag gaa gat gat cgc tat tac aca gct atc aat ttt gtg gct 3552  
 Leu Ser Gln Glu Asp Asp Arg Tyr Tyr Thr Ala Ile Asn Phe Val Ala 1180  
 1170 1175  
 act cct gac gaa caa aac agg gat ttg gac atg ttc atc aat gcc tcc 3600  
 Thr Pro Asp Glu Gln Asn Arg Asp Leu Asp Met Phe Ile Asn Ala Ser 1195  
 1185 1190  
 aag aat ttc aac ctc aac atc acc tgg gct gcc agt ttc tca gct gga 3648  
 Lys Asn Phe Asn Leu Asn Ile Thr Trp Ala Ala Ser Phe Ser Ala Gly 1215  
 1205 1210  
 acc cag gct gga gaa gag atg cct gtt gtt tca aaa acc aac att aag 3696  
 Thr Gln Ala Gly Glu Glu Met Pro Val Val Ser Lys Thr Asn Ile Lys 1230  
 1220 1225  
 gag tac aaa gat agt ttc tct aat gag aag ttt gat ttt cgc aac cac 3744  
 Glu Tyr Lys Asp Ser Phe Ser Asn Glu Lys Phe Asp Phe Arg Asn His 1245  
 1235 1240  
 cca aat atc act ttc ttt gtt tat gtc agt aat ttc acc tgg ccc atc 3792  
 Pro Asn Ile Thr Phe Phe Val Tyr Val Ser Asn Phe Thr Trp Pro Ile 1260  
 1250 1255  
 aaa att cag gtg caa act gaa caa tga 3819  
 Lys Ile Gln Val Gln Thr Glu Gln 1270  
 1265 1270

<210> 20  
 <211> 17  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Cys Glu Val Glu Asn Arg Tyr Gln Gly Asn Pro Leu Arg Gly Thr Cys 15  
 1 5 10  
 Tyr

<210> 21  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 21  
 Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Cys 10  
 1 5

<210> 22  
 <211> 5  
 <212> PRT

```

<213> Homo sapiens
<220>
<221> VARIANT
<222> (1)...(4)
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (5)...(5)
<223> Xaa = Gly, Ser, or Ala

<400> 22
Gly Xaa Ser Xaa Xaa
 1          5

<210> 23
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (2)...(8)
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (9)...(9)
<223> Xaa = Leu, Ile, Val, Met, Phe, Tyr, or Trp

<221> VARIANT
<222> (10)...(29)
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (30)...(30)
<223> Xaa = Leu, Ile, Val, Met, Phe, Tyr, or Trp

<400> 23
Asp Xaa Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1          5          10          15
Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Ser Xaa Gly Gly Xaa
      20          25          30

<210> 24
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (3)...(4)
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> (6)...(6)
<223> Xaa = Asp or Glu

<221> VARIANT
<222> (9)...(9)
<223> Xaa = Gly or Ser

<400> 24
Ala Ala Xaa Xaa Gly Xaa Ser Gly Xaa Pro His
 1          5          10

```

```

<210> 25
<211> 10

```

WO 00/15651

PCT/US99/20948

35

<212> DNA  
<213> Homo sapiens

<400> 25  
gggaagatgg

10